Novel nucleotide s Coding sequence fo Polynucleotide seq Homo sapiens 20q13 Human PRO274 nucle Human RNA helicse Coding strand of Human LOBO homolog C kappa exon prime	Plant microsatelli Human Colon cancer Immunogen DNA from Human 5 EST isola Murine BC1-2 inter Human secreted pro Murine BC1-2 inter Plant microsatelli Plant microsatelli Plant microsatelli Calcium ion channe Murine BC1-2 inter EST clone BN180. Clone GN156 encodi Streptococcus pneu MAGE-4 encoding ge H6/MAGE-1 expressi H6/MAGE-1 expressi	H6/MAGE-1 expressi H6/MAGE-1 expressi Hman secreted pro Hepatitis C virus Hepatitis C virus Hepatitis C virus NANB hepatitis vir CDNA encoding a fo CLYTA MAGE-1-His f Lipoprotein D-MAGE 165 RNA from ATCC CDNA encoding prot DNA encoding grot DNA encoding GTP-b Streptococcus pneu Neursodegenerative Murine D6 encoding Mouse FAST-1 codin Tumour rejection a Human prostate tum Beta(1 -> 4)·N-ace DNA encoding human Human HCDR-1 codin Human HCDR-1 codin Human TRAF four as	HILUDUOU TACETORED B H
0.6 1626 20 0.6 2450 20 0.6 2450 20 0.6 2605 19 0.6 4120 20 0.6 4139 19 0.6 4139 19 0.6 4999 20 0.6 6139 19 0.6 6200 20 0.6 62	0.6 300 21 0.6 300 21 0.6 300 21 0.6 300 21 0.6 300 21 0.6 426 21 0.6 426 21 0.6 550 10 0.6 550 10 0.6 1022 20 0.6 1022 20 0.6 1022 20 0.6 1022 20	17 0.6 1094 15 067865 17 0.6 1094 20 X208441 17 0.6 1140 20 X208441 17 0.6 1173 13 029634 17 0.6 1173 14 029635 17 0.6 1173 14 029635 17 0.6 1338 21 2466089 17 0.6 1341 20 X87591 17 0.6 1345 12 014450 17 0.6 1557 17 727644 17 0.6 1592 19 V42963 17 0.6 1688 20 V72116 V17 0.6 1688 20 V72116 V17 0.6 1688 20 V72116 V17 0.6 1688 20 V72116 V17 0.6 1724 19 V383876 V17 0.6 11816 20 X885940 V17 0.6 1816 20 X85594 V17 0.6 1816 20 X85550 V17 0.6 1816 20 X85594 V17 0.6 1816 20 X85594	0.6 2418 20 0.6 2419 13 0.6 2419 15 0.6 2419 15 0.6 2419 16 0.6 2419 16 0.6 2420 15 0.6 2971 9 0.6 3156 19 0.6 3156 19 0.6 3156 19 0.6 3457 14 0.6 4216 8 0.6 4216 8 0.6 4488 14
4.5 Compugen Ltd. Compugents Compu	ataaagattgagtttgcaa 2958	eqn/NA1980.DAT:* eqn/NA1981.DAT:* eqn/NA1981.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1982.DAT:* eqn/NA1980.DAT:* eqn/NA1990.DAT:* eqqn/NA1990.DAT:*	to have a being printed, being gene signatu tuman biallelic po ser and ser a
GenCore version 4.5 Copyright (c) 1993 - 2000 Compus M nucleic - nucleic search, using sw model The responsible of the search of	Title: Derfect score: 2958 Sequence: 1 cgcggcgtaggtgaccggca Scoring table: 0LIGO_NUC Gapop 60.0 , Gapext 60.0 Searched: 480022 seqs, 187831343 residues Acrd size: 0 Stal number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Listing first 100 summaries	4400004444444444	Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribut and is derived by analysis of the total score distribut and is derived by analysis of the total score distribut score distribut and is derived by analysis of the total score distribut score distribut and is derived by analysis of the total score distribut score distribut score distribut and is desired by analysis of the total score distribut score distribut score distribut and is desired by analysis of the total score distribut and is desired by analysis of the total score distribut and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score of the result and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the total score distributant and is desired by analysis of the

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MAGE-1 nucleic aci	Tumour rejection a	MAGE-1 gene. Homo	Lats gene encoding	Drosophila melanog	Tumour rejection a	Arylamine N-acetyl	Streptococcus pneu	Polynucleotide seq	Staphylococcus aur	Rat nestin gene -	Polynucleotide seq	Partial mouse WRN	Complete nucleotid	Human METH1 relate
032352	072477	X84113	T42117	251508	098902	048772	V52165	X20553	V74675	070447	X20535	x83005	230163	Z32020
13	15	20	17	21	16	14	19	20	18	15	20	18	20	20
5674	5674	5674	5720	5720	5724	6464	10240	10461	10813	11236	21170	29604	34094	38734
9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0
17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
86	87	88	83	06	91	92	93	94	95	96	2 97	86	66	2 100

ALIGNMENTS

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Z80231 standard; cDNA; 238 BP
ESULT
 30231
    윤본<mark>당본틳첮밁첮뮭촞풑춙잗삤첮來</mark>춖굒궦춖궦잗궦똣궦잗궦뭙作첮뺚첮뫢뭙믮캶먑먑먑먑먑먑먑먑땹
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280231;

(first entry)

07-APR-2000

Human colon cancer cell line SW480 cDNA clone SEQ ID NO:315.

cancer; Human; gene expression product; diagnosis; tumour; colon cancer. colorectal adenocarchnoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.

Homo sapiens

W09964576-A2

16-DEC-1999

99WO-IB01062 09-JUN-1999; 98US-0088801 10-JUN-1998;

(FARB) BAYER CORP

Monahan JE; 2, Astle JH, Burgess CC, Bushnell Derti A, Ford DM, Lewis ME, Monah Steinmann KE, Catino IJ, D Endege WO, Carroll E, Schlegel R;

WPI; 2000-087220/07

Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer

Claim 15; Page 258; 469pp; English.

Any solution to 280766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The colon clones can be used to generate antisense oligonucleocides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders. Involving unwanted cell proliferation, such as neoplasia, dysplasia or hyperplasia

Sequence 238 BP; 55 A; 57 C; 69 G; 57 T; 0 other;

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double-stranded DNA, which comprises one of the 7837 "GS" sequences glouble-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T2687 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-confincted cDNAs hybridise with specific mRNAs beaches almost all the 3'-criented cDNAs hybridise with specific mRNAs. Each library is confirtucted so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS. sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                  226 acctgcaggtggtggcagcgggtagccgggactcgggcgccgcgctctacgtcttctccg 285
                                                                                                                                                                                                    405
                                                                                                                                                                                                                                   121 agttaaaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttg 180
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frequency;
                                                                                                                                                                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                    agttaaaggttgctcgcctggacaacatattcctgacagaatgcactggtctaatgttg
                                                                                                    1 acctgcaggtggtggtagcagggtagccggggactcggggcgccgcgctctacgtcttctccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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 Length 238;
                                  Indels
                 4.1e-106;
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 DB 21;
8.0%; Score 237; DE 100.0%; Pred. No. 4.1 iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     T25953 standard; cDNA to mRNA; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene signature HUMGS08188
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 Query Match 8.0°
Best Local Similarity 100.
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-206931/27
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Gaps

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Length 72; Indels

DB 16; Le 4.4e-16; hes 0;

71

Length 68;

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Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
                                                                                                                   Human biallelic polymorphic DNA fragment ESTC169.
                         Seguence 72 BP; 25 A; 10 C; 16 G; 20 T; 1 other;
                                                                  1.8%; Score 53; DB 100.0%; Pred. No. 4.4 tive 0; Mismatches
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recognising different cell types.
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                                                                                                                                                                                                                                                                       (first entry)
                                                                                            Conservative
                                                                                                                                                                                                     34/c
X11554 standard; DNA; 68
                                                                                                                                                                                                                                                                                                                                                                  treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-286974/25.
                                                                  Query Match
Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9820165-A2
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                            X11554;
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X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aidrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic Kidney disease, hereditary spherocytosis, von Willebrand's disease, hereditary shaemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such endurance, fertility and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid proporty such diseases. such diseases

Sequence 68 BP; 12 A; 13 C; 21 G; 21 T; 1 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an expressed sequence tag (EST), and is a polyuncleotides of the invention. The polyuncleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to thave useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haemostatic activity, haemostatic
                                                                                                                                                                                                                                                                                                            Expressed sequence tag; secreted protein; haematopoiesis regulator; issue growth; activin; infilblin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostaxis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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100.0%; Pred. No. 18;
                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy JM,
                                                                         tggaaacagacggcggcacctttcctctaatccagcaaa 2850
         DB 19; L
3.1e-09;
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                                                                                         62 TGGAAACAGACGGCGCACTTTCCTCTAATCCAGCAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity. The EST sequences are also stated to
1.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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Treacy M;
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                                                                                                                                                                                   V88751 standard; cDNA; 526
                                                                                                                                                                                                                                                12-FEB-1999 (first entry)
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                                          Conservative
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070078/06.
                           Similarity
                                                                                                                                                                                                                                                                               EST clone HK189
        Query Match
Best Local Simi.
Matches 39;
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P-PSDB; W89417, W89418, W89419, W89420
                                                                       Claim 8; Fig 4A-4P'; 202pp; English.
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                                                                                                                                                                                                                                                                                                                                                                          811 tcttggtgctcaaagcaaa 829
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98US-0078886.
98US-0078910.
98US-0078936.
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98US-0077791
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                                                                                                                                                                                                                                                            the lower respiratory
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Z33905 standard; DNA; 45
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Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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11-MAR-1998;
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                                                    infections
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   δλ
                                                                                                                                                                                                                                                                                                             /transl_except= (pos:509..512, aa:Asp)
/note= "this codon has an apparent 1 codon
insertion, which alters the reading frame"
/note= "lbpB is specifically claimed in Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= i
/*tag= i
/gene= lbpA
/product= LBP1
/note= "specifically claimed in claim 8; encodes
W89419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene- orf3
/note- "specifically claimed in Claim 7; encodes W89419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product=^LBP1
/note= "specifically claimed in Claim 8; encodes
w89418"
                                                                                                                        Lactoferrin receptor; lactoferrin binding protein; LBP1; LBP2; lbpA gene; lbpB gene; ORF3; infection; otifits media; sinusitis; conjunctivitis; pneumonia; bronchitis; tracheitis; anhysema; diagnosis; therapy; vaccine; Branhamella catarrhalis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Q,
                                                                                                                                                                                                                                                                                                                                                     encodes W89417
                                                                                                      Moraxella catarrhalis Q8 lfr region.
                                                                                                                                                                                                Location/Qualifiers 90..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du R, Klein MH, Loosmore SM,
                                                                                                                                                                                                                                                                                                     'product- LBP2
                                         V82020 standard; DNA; 7642 BP
                                                                                                                                                                                                                            108..113
/*tag= b
138..147
/*tag= c
/*tag= c
/*tag= d
/*tag= d
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97US-0867941.
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//...3016
/*tag= __
/22
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/gene= lbpA
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2991..2996
                                                                                  21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                              2974..2979
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                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                             Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-070266/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
03-JUN-1997;
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                                                                                                                                                                                               Key
-35_signal
                                                                                                                                                                                                                            -10_signal
                                                                                                                                                                                                                                                                                                                                                                                   -10_signal
                                                                                                                                                                                                                                                                                                                                                                 -35_signal
                                                              V82020;
                                                                                                                                                                                                                                                                                                                                                                                                       RBS
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                                                                                                                                                                                                                                                   RBS
                       SOLT
                              :32020
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This polynucleotide comprises the lactoferrin receptor (lfr) locus of Moraxella catarrhalis (Branhamella catarrhalis) Q8. There are 3 tandem genes in locus, identified as lbpA, lbbB (alternative protein 2 (lbp2, see WB941), lactoferrin binding protein 1 (lbp1, protein 2 (lbp2, see WB941), lactoferrin binding protein 3 (DRF3, see WB9420). The lfr locus was identified following generation of a M. catarrhalis strain Q8 genomic DNA library and screening with specific hybridisation probes. The genes and DNA sequences of the granton of diagnostis, immunisation, and the compositions, including vaccines, based upon expressed recombinant compositions, including vaccines, based upon expressed recombinant club, and/or Lbp2 and/or ORF3, portions of these or their analogues, can be prepared for prevention of diseases caused by Moraxella. M. catarrhalis is a causative agent of otitis media and has been associated with sinusitis, conjunctivitis and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; center; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Lactoferrin receptor genes from Moraxella, especially M. catarrhalis - useful to diagnose Moraxella infection e.g. to detect otitis media due to M. catarrhalis infection and to immunise against such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Length 7642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tract, such as pneumonia, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7642 BP; 2417 A; 1726 C; 1631 G; 1868 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. 18;
iive 0; Mismatches
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secreted and transmembrane polypeptides and their polynucleotides, ful for treating blood coagulation disorders, cancers and cellular

Example 4; Page 184; 530pp; English.

adhesion disorders

nseful

Chen

Baker KP,

Yuan

Gurney A,

Goddard A,

Wood WI,

WPI; 1999-551358/46.

(GETH) GENENTECH INC

98US-0087098. 98US-0087106. 98US-0087208. 98US-0094651. 98US-0100038.

28-MAY-1998, 30-JUL-1998, 28-MAY-1998 28-MAY-1998

11-SEP-1998

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98US-0078939.
98US-0079294.
98US-0079656.
98US-0079663.
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300-sn86
800-sn86
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                                                                                                                                                                                                                                                                                          The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. 233891 to 234338, and Y41885 to Y41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastro-intestinal transport receptor; binding protein; hSI; HPTl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lambkin IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding sequence for human SI binding protein SNi45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB;
Pred. No. 60;
0; Mismatches
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, Singleton J;
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100.0%; Pr:
0;
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X18066 standard; DNA; 177 BP
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Patterson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTO-) CYTOGEN CORP. (ELAN-) ELAN CORP PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09851325-A2.
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Omahony DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         x18066;
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X18066/
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vaccines to treat or prevent H. pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: This DNA sequence is not reproduced in the specification and has been derived from the related specification, WO9719098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunisation; detection; antisense; inhibition; cytoplasmic; Na+/H+ antiporter; Escherichia coli; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a Helicobacter pylori cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 18; DB 18; Length 531;
100.0%; Pred. No. 57;
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/transl_except= (pos: 520..522,
/transl_except= (pos: 526..528,
/note= "xaa = Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cytoplasmic protein ORF 24824087.aa.
                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences
                                                                                                        Mellgaerd BL;
                                                                                                                                                                                                                                                                       polypeptide(s) - useful for vaccines
infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..531
                                                                                                                                                                                                                                                                                                                                                Claim 9; Page : 1481pp; English.
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100.0%; Prt
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95US-0487032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                           Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
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                                                                                                                                                                 WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity.
Matches 18; Conserva
                                                     (ASTR ) ASTRA AB.
                                                                                                                                                                                             P-PSDB; W20335.
                                                                                                           Berglindh OT,
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9719098-A1
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T77453/c
This sequence encodes a peptide that specifically binds to the human sucrose-isomaltase complex. The invention relates to purified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal decisions associated transporter (HPII), hPEPTI, DZH and human peptide-associated transporter (HPII), hPEPTI, DZH and human sucrose-isomaltase complex (HSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migrathe, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) ane (I) are (I) to determine the level of specified receptors in a sample (in a binding assay); and (ii) to screen for molecules that bind (I). Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunosasys. The antibodies are used to locate, detect and massing the provided target are used to locate, detect and massing of the information of the content of an immunosasys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ing treatment, tissue analysis
                                                  New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimmeras and antibodies, used to deliver therapeutic or diagnostic agents to, or through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; prevention; treatment; infection; identification;
binding compound; bacterium; life cycle; activator; bacteria;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 58;
0; Mismatches 0; Indels
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Xaa)
Xaa)
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a a a ...
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/transl_except= (pos: 520..522,
/transl_except= (pos: 526..528,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori cytoplasmic protein ORF 24824087.aa.
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                                                                                                                                                                                             Claim 49; Page 56; 294pp; English.
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/note= "Xaa = Un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%; SC
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESULT 8
T67773/c
T0 T67773 standard; DNA; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..531
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori.
WPI; 1999-009568/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytoplasmic; ds
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T67773;

1528888888888898991

Gaps

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Indels

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Smith DH;

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279917 to 280766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inositol 1,3,4-triphosphate 5/6-kinase; phytic acid; genetic mapping;
myo-inositol 1,2,3,4,5,6-hexaphosphate; biosynthetic enzyme; phytate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                                                                                                                                                                                                                                                                  Astle JH, Burgess CC, Bushnell SE;
rti A, Ford DM, Lewis ME, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean inositol 1,3,4-triphosphate 5/6-kinase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 21; Length 726;
Pred. No. 57;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 726 BP; 149 A; 157 C; 170 G; 198 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 462; 469pp; English.
                                                                                                                                                                                                                                                                                                                                  Derti A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; SCO.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z48812 standard; cDNA; 1040 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US08790.
                                                                                              99WO-IB01062.
                                                                                                                                                                 98US-0088801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                  Steinmann KE,
Catino TJ, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-087220/07.
                                                                                                                                                                                                                                   (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal feed; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09955879-A1
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                                                                                              09-JUN-1999;
                                                                                                                                                                 10-JUN-1998;
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                            16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperplasia
                                                                                                                                                                                                                                                                                                                                     Carroll E,
Schlegel R;
                                                                                                                                                                                                                                                                                                  Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragments were blunt-ended and ligated to unique BstXI-linker addapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linker-adapter inserts were ligated to each of the 20 pMpX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori nucleic acid sequences and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a Helicobacter pylori cytoplasmic protein, which was found to be homologous to Escherichia coli Na+/H+ antiporter protein following BLAST protein analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The ORF/protein reference number for this sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer cell line SW480 cDNA clone SEQ ID NO:833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ore 18; DB 18; Length 531;
red. No. 57;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 531 BP; 175 A; 88 C; 114 G; 151 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obtained from the related specification, WO9640893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 100; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280749 standard; cDNA; 726 BP
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                                                               96WO-US18542
                                                                                                                                 95US-0561469
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                                                                                                                                                                                                                                                                                                                                  WPI; 1997-298052/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                    (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; W24635
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                                                               15-NOV-1996;
29-MAY-1997
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Gaps

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Pearlstein RW;

Hitz WD,

Carlson TJ,

Cahoon RE,

WPI; 2000-072179/06

(DUPO') DU PONT DE NEMOURS & CO E I.

hyperplasia; ds

280749;

ESULT 10 30749

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Note:

Homo sapiens W09964576-A2

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protein of the invention. TIK is a phytic acid (Mychinosittal 1/2,3,4,5,6-hexaphosphate) blosynthetic enzyme. The ITK enzymes of the invention may be prepared recombinantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides of the invention may be used to reacte transgenic plants in which the ITK levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of 1,3,4-triphosphate 5/6 kinase found in those cells. In addition, it may be desirable to eliminate expression of ITK genes for certain applications. The polynucleotides also serve as a source of probes and applications. The polynucleotides also serve as a source of probes and applications. Which are useful for genetic mapping, as markers for traits linked to those genes, and increased amounts of available phosphate in animal feeds such as corn would lead to improved feed efficiency. The proteins of the present invention lead to a better understanding of the phytic acid blosynthesis pathway, allowing it to be exploited for commercial uses, e.g. in animal
                                                   Novel phytic acid biosynthetic enzymes used to alter the level of the
                                                                                                                                                                                          This sequence encodes an inositol 1,3,4-triphosphate 5/6-kinase (ITK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1040 BP; 264 A; 255 C; 265 G; 256 T; 0 other;
                                                                                                                                   63pp; English.
                                                                                enzyme in transgenic plants
                                                                                                                                      Claim 2; Page 53;
P-PSDB; Y59428
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21; Length 1040;

Indels .; 0 Score 18; DB Pred. No. 56; Mismatches 0.6%; Scc. 100.0%; Pre 0; 990 gaaagcttcattcaaccc 1007 Query Match 0.6 Best Local Similarity 100. Matches 18; Conservative

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Gaps

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Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; H. pylori cytoplasmic protein ORF 06cp30603orf11.

/*tag= a /note= "no stop codon given" Location/Qualifiers

WO9640893-A1

96WO-US09122. 06-JUN-1996; 19-DEC-1996

96US-0630405. 95US-0487032. 01-APR-1996; 07-JUN-1995;

(ASTR) ASTRA

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The present sequence encodes a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORP of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                 Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide; protein; nutrition; cytokine; cell proliferation; cell differentiation; immunostimulation; immunosuppression; haematopoiesis regulation; tissue growth; activin; inhibin; chemotaxis; chemotaxis; haemostasis; thrombolysis; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand; anti-inflammatory; tumour suppression; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleotide sequence encoding new protein (Clone AC222_1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1593 BP; 541 A; 288 C; 334 G; 430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
56;
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Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Novel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 18; 00.0%; Pred. No.
 Smith D, 'Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                      Claim 9; Page 833; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0.,
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1760 aaagccgcttcacccttt 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1376 AAAGCCGCTTCACCCTTT 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X08683 standard; cDNA; 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ, Bowman M
McCoy JM, Merberg D,
                                   WPI; 1997-052306/05.
Berglindh OT,
                                               P-PSDB; W20739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X08683;
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X08683/c
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Gaps

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Gaps

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Indels

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Length 2186;

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the invention (the encoded protein is not given in the specification). The inhibitor is a Kexz proteinase family enzyme inhibitor with a molecular weight of 11,500. The inhibitor/protein (termed Kexstatin) is expected to have pharmaceutical and pesticidal applications.
                                              sequence is the coding sequence for an example of the inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X20500-21243 represent polynucleotide sequences from the genome of
Treponema pallidum. The sequences can be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                     Sequence 2186 BP; 297 A; 827 C; 780 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2450 BP; 553 A; 643 C; 631 G; 617 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                       Score 18; DB 19
Pred. No. 55;
0; Mismatches
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Pred. No. 55;
0; Mismatches
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Disclosure; Page 18-19; 29pp; English.
                                                                                                                                                                                                                                        0.6%; Scur
100.0%; Pre
0;
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                   1518 ggtcctgggcaccctggc 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20537 standard; DNA; 2450
                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                The new human secreted proteins are encoded by polynucleotides obtained from human placenta, adult testes, fetal kidney, fetal brain, adult brain and adult blood cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or amellorating medical conditions in humans and animals. Suggested
                                                                                                                                                                                                                                                                                                                         activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, immune stimulating (e.g. as activity, tissue growth activity, activity/inhibin activity, chemotactic/chemokinetic activity, activity/inhibin activity, activity, acceptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. The sequences are identified by a secretory leader sequence motif in the polynucleotide and it is thought that the encoded proteins have biological activity by virtue of their secreted mature. This clone was designated AC222_1. A probe for this clone is described in X08698.
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pesticidal applications
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                                                                                             New polynucleotides encoding secreted human proteins
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100.0%; Pred. No. 56;
Ive 0; Mismatches
                                                                                                                                         Claim 14; Page 101-102; 135pp; English
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100.0%; Pr
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96JP-0158677.
96JP-0224104.
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ses 18; Conserv
                                            P-PSDB; W85718
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19-JUN-1996;
26-AUG-1996;
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Query Match

Matches

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Gaps

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Length 2450; Indels

V04699;

ESULT 16 704699/c

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Human, PRO, EST, expressed sequence tag, PCR primer, hybridisation, probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                         Human PRO274 nucleotides sequence.
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98US-0078004.
98US-0040220.
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98US-0079689.
98US-0079728.
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98US-0081070.
98US-0081071.
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98US-0083392.
98US-0083495.
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98US-0080105
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98US-0080194
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98US-0081955
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98US-0082700
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98US-0080334
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                                          (first entry)
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98US-0081
98US-0081
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                 W09946281-A2.
                                          07-DEC-1999
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           Z33895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a cDNA sequence cc43, which was isolated from the 20q13 amplicon. It is expressed in normal tissues but not been found in the breast cancer cell line. It can be used as a probe for the detection of chromosomal abnormalities at 20q13. It and other sequences isolated from the 20q13 amplicon are consistently amplified in primary tumours. These sequences are useful as probes or as probe targets for monitoring the relative copy number of corresponding sequences from a biological sample such as tumour cells. The sequences can also be used in therapeutic applications for modulating the expression of the endogenous gene or the activity of the gene product. Examples of therapeutic approaches include antisense inhibition of gene expression, gene therapy, and monoclonal antisense inhibition of gene expression, gene products. The products can also be used in the treatment of other diseases, e.g. age-related macular degeneration, peber's congenital amaurosis and retnitis
                                                                                                                                                                  20q13 amplicon; chromosome 20; tumour; detection; chromosomal abnormalities; probe; gene therapy; antisense inhibition; treatment; age-related macular degeneration; retinitis pigmentation; Leber's congenital amaurosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New sequences from the 20q13 amplicon - used for detecting chromosomal abnormalities, particularly tumours, and for developing products for treating diseases
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100.0%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collins CC, Godfrey T, Gray JW, Hwang SI, Kowbel D;
Rommens J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2605 BP; 698 A; 625 C; 549 G; 732 T; 1 other;
                                                                                                                                      Homo sapiens 20q13 amplicon cc43 transcript.
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Matches 18; Conservative 0;
                                           V04699 standard; cDNA; 2605 BP
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96US-0680395.
96US-0731499.
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15-JUL-1996;
16-OCT-1996;
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98US-0083545. 98US-0083545. 98US-0083554.

SSULT 17 33895 2 233895 standard; cDNA; 2945 BP.

Query Match

(first entry)

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which contains a nucleic acid (1) that codes for a protein (II) of the DEAD-superfamily. (A), and recombinant insect viruses derived from them, are used to express recombinant (II), particularly RNA and DNA helicases. (II) are potentially useful for: (a) production of cell lines for research into cancer, inflammation and apoptosis, or for clarifying the mechanism of action of drugs, and (b) to identify pharmaceutical activity in known compounds, e.g. anticancer and antiviral activities. (II), which are difficult to express in bacteria and yeast, are expressed at high level in insect cells, e.g. 300-400 mg per 109 cells. This sequence encodes a human RNA-helicase pl35 protein which is used in the description of the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the construction of a novel insect cell vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insect cell vector containing the sequence encoding a DEAD-superfamily protein, particularly a nucleic acid helicase, used e.g. for identifying potential pharmaceuticals
                                                                                                                                                       DEAD protein; insect cell vector; DEAD-superfamily; RNA helicase; bNA helicase; cancer research; cell line; inflammation; apoptosis; drug; anticancer; antiviral; pl35; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 38-40; 43pp; German
                                                                                                                           Human RNA helicase p135 DNA #2.
    Z09473 standard; DNA; 4120 BP.
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                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                      WO9941390-A2
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Matches
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V70354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion, disorders. They may also be used to raise antibodies. 233891 to '33438, and Y41685 to Y41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.
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                                                                                                                         98US-0084598
                                                                                98US-0084414
98US-0084441
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P-PSDB; Y41686.
29-APR-1998;
29-APR-1998;
30-APR-1998;
05-MAY-1998;
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06-MAY-1998;
07-MAY-1998;
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99WO-EP00829. 98DE-1005781. Gallert K, Huels C, Muellner S;

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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer; detection; hK2; hK1; hK3; phK2; tissue kallikrein;
pphK2; prostate-specific glandular kallikrein protein; PSA; human;
                                                                                  ö
                                               Length 4120;
Sequence 4120 BP; 1099 A; 1021 C; 1236 G; 764 T; 0 other;
                                                                                  Indels
                                                                                  ..
                                                  20;
                                               DB .
                                                                                  Mismatches
                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                      Coding strand of native genomic hK2.
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                            prostate-specific antigen; ss.
                                                                                                                                                                                                                                      V70354 standard; DNA; 6139 BP.
                                                                  100.08;
                                                                                                                 1338 aggagggagtggcagagg 1355
                                                  0.68;
                                                                                                                                                  809 AGGAGGAGTGGCAGAGG 792
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                Local Similarity 100.
ses 18; Conservative
                                                                                                                                                                                                                                                                                            09-FEB-1999
                                                                                                                                                                                                                                                                      V70354;
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Gaps

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0; Indels

Length 2945;

0.6%; Score 18; DB 20; 100.0%; Pred. No. 55; Mismatches

0.00, 100.0%; Pr

18; Conservative

Matches

Best Local Similarity

Query Match

872 cattgctgctgtcaagga 889

2 .0 TESULT 18

Homo sapiens

WO9846795-A1

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kallfxrein 2 (hKZ) DNN. The method comprises: (a) contacting DNA obtained by reverse transcription (RT) of RNA from a human physiological sample which comprises cells suspected of containing hKZ RNA with at least 2 oligonuclectides to amplify the DNA by PCR to yield amplified hKZ DNA, where the conditions amplify the DNA obtained by RT of RNA from at least one cells; and (b) detecting the presence of the amplified hKZ DNA. The method can be used for detecting, monitoring the prospession of and pathologically staging prostate cancer. The present sequence represents the coding strand of native genomic hKZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a diagnostic method for detecting human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; human; ds.
                                                                                                                                                                                                                                                                                                                                                                  Detection of human kallikrein 2 RNA - by reverse transcription and amplification by PCR, for detecting, monitoring and staging of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 19; Length 6139;
Pred. No. 54;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6139 BP; 1233 A; 1875 C; 1595 G; 1436 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human LOBO homologue genomic DNA fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 78-80; 90pp; English.
                                                                                                                                                                                                                                                 Slawin KM, Tindall DJ, Young CYF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Scur
100.0%; Pre
0;
                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3/c
223903 standard; DNA; 49999 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 cagatgccccgtggcct 1065
                                                        98WO-US07027
                                                                                                             97US-0843076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98DE-1013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                               (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                            WPI; 1998-594592/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09950284-A2
                                                     09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1999.
22-OCT-1998.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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SSULT

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Gaps

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bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achodroplasia. This sequence encodes a human LOBO protein described
                                                                                                                                     novel nucleic acids (I; designated LOBO (long
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                          proteins which influence bone development,
                                                                                                                                                                                                                                                                                                                       Sequence 49999 BP; 10983 A; 13723 C; 13439 G; 11854 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homologous replacement of gene in mammalian germ line - by transfecting embryonic stem cell with labelled recombination vehicle, selection and incorporating into blastocyst(s) for implantation, esp. for prodn. of humanised antibodies in mice
                                                                                                                                                                                                                                                                                                                                                                  Length 49999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSM 7211 is made by (1) inserting a fragment of pC:2 (contg. the C kappa exon) into pTZ-19(R); (2) inserting a 1.2 kb fragment of pHBc kappa (contg. the intron enhancer element);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Germ line; stem cell; blastocyst; implantation; embryonic;
electroporation; kappa; constant; exon; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
Wirth T;
                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                          useful for treating and studying bone disorders
                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 2; Pred. No. 52; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RAJE/) RAJEWSKY K.
(KOEL-) KOELNER VER FOERDERUNG IMMUNOLOGIE
Aigner T,
                                                                                                       Example 3; Page 328-356; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                        0.6%; Sc._
100.0%; Pre
0;
Hess J,
                                                                                                                                                                                                                                                                                          in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Column 4; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 14820 GGGCCAGGAGGCTGCCAC 14803
                                                                                                                                                                                                                                                                                                                                                                                                                                 2740 gggccaggaggctgccac 2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92DE-4228162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q54684 standard; DNA; 21
                                                          acids encoding
Rosenthal A, Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-008862/02.
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C kappa exon primer.
                           WPI; 1999-601320/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zon X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE4228162-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                          Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       054684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
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Q54684
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Gaps

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Length 256; Indels

Score 17; DB 21; L Pred. No. 1.8e+02;

0.6%; SCUL 100.0%; Pre 0;

Conservative

Query Match Best Local Similarity Matches 17; Conserv

35 G; 91 T; 0 other;

Sequence 256 BP; 89 A; 41 C;

ΧX

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codon of this exon.

Shar 7211 was introduced into embryonic mouse stem cells by electroporation. Wild type mice have in their serum no antibodies carrying the human kappa gene constant region, but in mice homozygotic for the mutation, such antibodies were present at
(3) inserting a 1.1 kb fragment contg. the neomycin resistance gene of pMCIneo; (4) inserting the 2.8 kb fragment of pHJkappa (contg. the J1-5) elements); then (5) finally inserting a 427 bp fragment made by port mouse germ line DNA using one primer (054683) which hybridises 12 bp after the start of the C kappa exon and another (054684) which hybridises 137 bp after the stop
                                                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                   0.6%; Score 17; DB 15; Le
                                                                                                                                                                                                                                                    Sequence 21 BP; 8 A; 2 C; 10 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant microsatellite marker #1040.
                                                                                                                                                                                                                                                                                                               100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45SULT 22
-32079/c
-3 A32079 standard; DNA; 256 BP.
                                                                                                                                                                                                                                                                                                                                                                                     1031 gaggtaccaaggaaagg 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            1 gaggtaccaaggaaagg 17
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                             Query Match
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     888888888888888
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plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.

Pinus radiata W09967421-A1

Plant microsatellite marker #1011.

05-JUL-2000 (first entry)

A32050;

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Gaps

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A32050/c ID A32050 standard; DNA; 300 BP

RESULT 23

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Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant microsatellite markers and associated flanking species for detection of polymorphic genetic markers \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
(FLET-) FLETCHER CHALLENGE FORESIS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloksberg LN, Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-NZ00092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105307
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                                                                                                                                                                                                                                                                                                         Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                      WO9967421-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1999;
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YOUR TRANSPORT OF THE T
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plant microsatellite markers and associated flanking species for detection of polymorphic genetic markers

Claim 1; Page 373; 392pp; English.

(GENE-) GENESIS RES & DEV CORP LID & FLEICHER. (FLET-) FLETCHER CHALLENGE FORESTS LTD

99WO-NZ00092. 98US-0105307

25-JUN-1999; 25-JUN-1998;

29-DEC-1999.

Glenn M;

Bloksberg LN,

Havukkala IJ,

WPI; 2000-116958/10.

New the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonuclectide fingerprinting and library screening and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful to locate specific economically useful genes in plant genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for microsatellite-primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 17; DB 21; Length 300;
100.0%; Pred. No. 1.8e+02; 
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 300 BP; 99 A; 45 C; 43 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.1
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primers
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and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluations of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.

Sequences. A31040-A32093 represent novel plant microsatellite sequences

Claim 1; Page 382; 392pp; English.

Non-A, non-B, non-C, non-D, non-E hepatitis virus MY 190 clone

95WO-US05980

17-MAY-1995;

30-NOV-1995.

non-D, non-E hepatitis virus; n-(ABCDE); vaccine; phage library; ds.

Non-A, non-B, non-C, immunogen; antibody;

Non-A,

WO9532290-A2.

Immunogen DNA from n-(ABCDE) hepatitis virus.

(first entry)

05-JUL-1996

T07238;

T07238/c ID T07238 standard; DNA; 304 BP.

RESULT 25

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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                         Human colon cancer cell line polynucleotide sequence SEQ ID NO:1373.
                                                                                                                                                                           Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300 BP; 42 A; 104 C; 84 G; 70 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escobedo J, Innis ra:
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                                   A01382 standard; cDNA; 300 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0085537
98US-0085696
                                                                                                                                                                                                                                                                                                                                                                          99WO-US10602
                                                                                                                                                                                                                                                                                                                                                                                                            98US-0085426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105234
98US-0105877
                                                                                                          19-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams LT, Escobedo
Reinhard C, Giese K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-126369/11
                                                                                                                                                                                                                                                                                                       W09958675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                         18-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamson G,
                                                                        A01382;
.ESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells
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Labat I;

Sudduth-Klinger J; Pot D, Kassam A;

, García PD, Kennedy GC,

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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                            New non-A, -B, -C, -D and -E (n-(ABCDE)) hepatitis DNA libraries - used to develop prods. for the detection, diagnosis, prevention and treatment of n-(ABCDE) hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide associated with non-A, non-B, non-C, non-D, non-E hepatitis virus (n-(ABCDE) virus) infection, and is obtained by preparing a phage from a phage lambda gill library of MY 190 DNA (ATCC 75284) n-(ABCDE) hepatitis serum, plating to form plaques, and screening the phage plaques for the production of polypeptides immunoreactive with n-(ABCDE) serum. n-(ABCDE) hepatitis virus polypeptides can be used for the production or detection of antibodies, and in vaccines. The antibodies can be used for detection, diagnosis and in passive immunotherapy. The DNA can also be used in detection and diagnosis, and as hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes for identification of further n-(ABCDE) hepatitis coding sequences. Culture systems producing the n-(ABCDE) polypeptides can be used in screening studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents clone D30 which encodes an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 304;
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Pred. No. 1.8e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 304 BP; 65, A; 93 C; 94 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                             GENELABS TECHNOLOGIES INC.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 101; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; SCC.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z42643 standard; cDNA; 330 BP.
                                                                                                                                                                                                                                                   94US-0246986.
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                                                                                                                                                                                                                                                                                                                       Kim JP, Purcell RH;
                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-020585/02.
                                                                                                                                                                                                                                                   20-MAY-1994;
                                                                                                                                                                                                                                                                              GENE-)
                                                                                                                                                                                                                                                                                              ( HSSD)
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242643/C
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Gaps

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0.6%; Score 17; DB 21; Length*300; .00.0%; Pred. No. 1.8e+02; .ve 0; Mismatches 0; Indels (

100.0%; Pr tive 0;

Conservative

Query Match Best Local Similarity Matches 17; Conserv

2633 ccaggaggcagctcagg 2649

188 ccaggaggcagctcagg 204

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squences, corresponding to human secreted proteins. Y64651 to Y65438

represent the EST-related proteins corresponding to 24226 to 243052.
The S ESTs can be used for producing secreted human gene products.
They can be used to identify and isolate 5' untranslated regions (UTRS) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of mew secreted proteins is valuable. Z42249 to a valuation of the present sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                     Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification; ss.
Human 5' EST isolated from a cDNA library SEQ ID NO:402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242265 to 243075 represent novel 5' expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 330 BP; 76 A; 102 C; 86 G; 65 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A, Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 382; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0057719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-038446/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; Y65029
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                     WO9953051-A2
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28-APR-1998;
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   Length 330;
                                 0; Indels
0.6%; Score 17; DB 21; I 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0;
Query Match
Best Local Similarity 100.(
Matches 17; Conservative
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1219 acctcatccacccggac 1235 48 ACCICAICCACCGGAC 32:

:ESULT 27 %24993/c 72 X24993 standard; cDNA; 332 BP.

X24993;

05-JUL-1999 (first entry)

Murine Bc1-2 interacting mediator of cell death Bim-S cDNA.

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Gaps

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Indels

0.6%; Score 17; DB 20; Length 332;

1.8e+02;

Query Match 0.6%; Scc Best Local Similarity 100.0%; Pr Matches 17; Conservative 0;

Mismatches Pred. No.

Sequence 332 BP; 87 A; 85 C; 91 G; 69 T; 0 other;

preventing generation of fertile sperm.

The present sequence encodes the short form (5) of murine Bim, or Bc1-2 interacting mediator of cell death (see W98154), a novel member of the Bc1-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bc1-2 family. Bim is a BH3-only protein, as the colly Be1-2 homology region which it encompasses is BH3. It is the colly BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim.5, Bim.1 and Bim.EL (see W98154-56). cDNAs encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human recombinant Bc1-2 protein. The murine Bim gene has been mapped to chromosome 2 at bands F3-G. Human Bim.L and Bim.EL isoforms have chain was shown to regulate the pro-apoptotic activity of Bim. Bim.5, the splice variant which does not bind to dynein light chain, is a much more potent killer than either Bim.L or Bim.EL. The invention provides variants (see W98159-68) of murine and human Bim.L or Bim.E. that cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the identification and rational design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antendands and involving modulation as either antendands. useful in cancer, autoimmune or degenerative disease therapy.
Increased Bine expression or Bim activity is useful, e.g. for
treatment or prophylaxis in conditions such as cancer and deletion
of autoreactive lymphocytes in autoimmune disease. Decreased Bim
expression of Bim activity is useful in regulating inhibition or
prevention of cell death or degeneration such as under cytotoxic
conditions during e.g. gamma-irradiation and chemotherapy or during
HIV/AIDS or other viral infections, isohemia, myocardial infarction. hypoxia, degenerative diseases or for prolonging the survival of cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity New isolated member of the Bcl-2 family, Bim used in, e.g. cancer is useful; e.g. as a contraceptive or method of sterilization by cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant; 3im-S; Bcl-2 interacting mediator of cell death; apoptosis; O'Connor L, O'Reilly L; (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. Claim 3; Page 92; 145pp; English. Adams J, Cory S, Huang DCS, Puthalakath H, Strasser A; 98WO-AU00772. 97AU-0009373. 97AU-0009263. WPI; 1999-244030/20. P-PSDB; W98154. W09914321-A1 17-SEP-1998; Mus musculus 24-SEP-1997; 17-SEP-1997; isoform; ss. 25-MAR-1999 treatment Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.

98WO-IB01238

31-JUL-1998;

11-FEB-1999.

Homo sapiens. W09906554-A2

Human secreted protein 5' EST SEQ ID NO: 217.

(first entry)

18-JUN-1999

X41005 standard; cDNA; 369 BP

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA hybridise with specific mRNAs pacies, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                  Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 347 BP; 61 A; 102 C; 108 G; 75 T; 1 other;
                                                                                                 TESULT 28
24629
TO T24629 standard; cDNA to mRNA; 347 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1655; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognising different cell types.
                                                                                                                                                                                                                                                              Human gene signature HUMGS06689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0355504.
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654 aggecteteageagget 670
                                                                                                                                                                                                                          (first entry)
                   Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1994;
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                                                                                                                                                                                                                          07-0CT-1996
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                                                                                                                                                                                    T24629;
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**X40826 to X41093 represent 5' expressed sequence tags (ESTS) for human secreted proteins, and encode the proteins given in Y01602 and Y11994 to Y12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used for products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoissis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokanchic activity, haemastepic activity, tumour inhibition activity or other activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity anti-inflammatory. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
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Pred. No. 1.8e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 314-315; 622pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pr
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ID X24994 standard; cDNA; 422 BP.
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Best Local Similarity
Matches 17; Conserva
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P-PSDB; Y12172.
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:0; :Gaps : 0;

0.6%; Score 17; DB 16; Length 347; 100.0%; Pred. No. 1.8e+02; 1ve 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 17; Conservative

Query Match

15 ccaggagggagtggcag 31

ESULT 29

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Bim-L; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle, mouse; cancer; autolmmune disease; degenerative disease; therapy; contraceptive; splice variant; isoform; ss.
                                                                   Murine Bcl-2 interacting mediator of cell death Bim-L cDNA.
(first entry)
05-JUL-1999
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98WO-AU00772. 97AU-0009373. Mus musculus W09914321-A1 24-SEP-1997; 17-SEP-1997; 17-SEP-1998; 25-MAR-1999

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

97AU-0009263.

O'Connor L, O'Reilly L; Adams J, Cory S, Huang DCS, Puthalakath H, Strasser A;

WPI; 1999-244030/20. P-PSDB; W98155.

New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment

Claim 3; Page 94-95; 145pp; English.

The present sequence encodes the long form (L) of murine Bim, or member of the Bal-1 family that is capable of inducing cell death (see W98155), a novel member of the Bal-1 family that is capable of inducing cell death apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bal-2 family. Bim is a BH3-only protein, as the only BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim-S, and Bim-EL (see W98154-56). CDNAs encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human recombinant Bal-2 protein. The murine Bim gene has been mapped to carombosome 2 at bands F3-G. Human Bim-L and Bim-EL isoforms have also been identified (see W98157-58). Binding the dynein light chain was shown to regulate the pro-apoptotic activity of Bim. Bim-S, the splice variant which does not bind to dynein light chain, is a much more potent killer than either Bim-L or Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the identification and rational design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity is useful, and repression or Bim activity is useful, and season of autoreactive lymphocytes in autoimmune disease. Decreased Bim carterion of autoreactive lymphocytes in autoimmune disease. Decreased Bim carterion of cell death or degeneration and chemotherapy or during conditions during e.g. gamma-irradiation and chemotherapy or during the degeneration and chemotherapy and degeneration and chemothera cells being transplanted for treatment of disease. Since Bim is, expressed in germ cells, modulating Bim expression or Bim activity is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm. degenerative diseases or for prolonging the survival of

Sequence 422 BP; 112,A; 116 C; 109 G; 85,T; 0 other;

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Gaps

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0.6%; Score 17; DB 21; Length 426; 100.0%; Pred. No. 1.8e+02; live 0; Mismatches 0; Indels

RESULT

Query Match
Best Local Similarity 100.0
Matches 17; Conservative

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Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32095 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for
                                                                                                                                                                                                                                                                                                                                         Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New plant microsatellite markers and associated flanking species {\hbox{\it for}} the detection of polymorphic genetic markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes
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 Length 422;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 426 BP; 124 A; 81 C; 71 G; 150 T; 0 other;
Score 17; DB 20; L
Pred. No. 1.8e+02;
); Mismatches 0;
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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Havukkala IJ, Bloksberg LN, Glenn M;
                                                                                                                                                                                                                                                                                                    Plant microsatellite marker #1030.
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   0.55,
100.0%; Pre-
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                                                                        654 aggceteteageagget 670
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                                                                                          Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pinus radiata
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Location/Qualifiers

A32052;

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence. especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design
                                                                                                                                                  Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New plant microsatellite markers and associated flanking species for the detection of polymorphic genetic markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful to locate specific economically useful genes in plant genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium ion channel alphal subunit; human; episodic ataxia type 2; familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis; exon; intron; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primers for microsatellite-primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6%; Score 17; DB 21; Length 431; D.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 431 BP; 129 A; 78 C; 71 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.8
Mismatches
                                                                                                                   Plant microsatellite marker #1013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 374; 392pp; English.
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.32052/c
:2 A32052 standard; DNA; 431 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloksberg LN,
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                                                                                                                                                                                                                                                                                                                      99WO-NZ00092
                                                                                                                                                                                                                                                                                                                                                      98US-0105307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2021 tggctggaaagtggtct 2037
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 TGGCTGGAAAGTGGTCT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-116958/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Havukkala IJ,
                                                                                                                                                                                                                     Pinus radiata
                                                                                   05-JUL-2000
                                                                                                                                                                                                                                                    W09967421-A1
                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                    25-JUN-1998;
                                                                                                                                                                                                                                                                                     29-DEC-1999
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calcium ion channel alpha 1 subunit gene and part of untranslated calcium ion channel alpha 1 subunit gene and part of untranslated sequences. The channel is related to familial hemiplegic migratine (FHM) calcium ion channel is related to familial hemiplegic migratine (FHM) associated with a gene present in humans on chromosome 19p13.1-13.2. The encoding gene can be used to localise or identify genes related to or episodic neurological disorders, specifically migraine, FHM or EA-2, but also epilepsy. The isolated or a recombinant nucleic acid can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM.

EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to diagnose FHM, EA-2, migraine and other neurological conditions associated with cation channel disfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences shown in V29330 to V29371 represent the 47 exons and flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human nucleic acid associated with migraine and episodic ataxia type 2 - useful for diagnosis and development of specific treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terwindt GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 17; DB 19; 1
100.0%; Pred. No. 1.8e+02;
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                  'number= 32
'note= "partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ophoff RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 157pp; English.
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X24995/c
ID X24995 standard; cDNA; 590 BP.
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Matches 17; Conservative 0
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                                                                                                                                      'number= 33
                                                                                                                                                                                                                           'number= 33
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V29360;

TESULT 33

Matches

Sequence 590 BP; 137 A; 178 C; 150 G; 125 T; 0 other;

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Bim-EL, Bcl-2 interacting mediator of cell death; apoptosis, cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                  interacting mediator of cell death Bim-EL cDNA
                                                  (first entry)
                                                                                                     Murine Bcl-2
                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                W09914321-A1
                                                  05-JUL-1999
                                                                                                                                                                                                                                  isoform; ss.
                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999
X24995;
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O'Connor L, O'Reilly (HALL-) HALL INST MEDICAL RES WALTER & ELIZA Huang DCS, Adams J, Cory S, Huang DC: Puthalakath H, Strasser A;

97AU-0009373. 97AU-0009263. 98WO-AU00772

17-SEP-1997;

17-SEP-1998; 24-SEP-1997; ij

WPI; 1999-244030/20. P-PSDB; W98156 New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment

Claim 3; Page 96-97; 145pp; English.

The present sequence encodes the extra long form (EL) of murine Bim, or Bel-2 interacting mediator of cell death (see W88156), a novel member of the Bel-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bel-2 family. Bim is a BH3-only protein, as the only BH3-only protein for which splice variants exist. These only BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim-5, Bim-Land Bim-EL (see W98154-56). CDNAS encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human chromosome 2 at bands F3-G. Human Bim-EL and Bim-EL isoforms have also been identified (see W98157-58). Binding the dynein light chain was shown to regulate the pro-apoptotic activity of Bim. Bim-S, the splice variant which does not bind to dynein light chain, is a much more potent Killer than either Bim-L or Bim-EL.

The invention provides variants (see W98159-68) of murine and human Bim-L or Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The indentification of Bim permits the dentification and rational design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity is useful, e.g. for tradment or prophylaxis in conditions such as cancer and deletion of autoreactive lymphocytes in autoimmune disease. Decreased Bim expression of Bim activity is useful in regulating inhibition or prowntion of cell death or degeneration such as under cytocoxic conditions during e.g. amma-irradiation and chemotherapy or during HIV/AIDS or other viral infections, ischemia, myocardial infarction, cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity hypoxia, degenerative diseases or for prolonging the survival of is useful, e.g. as a contraceptive or method of sterilization by of disease. preventing generation of fertile sperm.

This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, and thrombolytic activity, receptor/ligand activity, the EST sequences are also stated to be useful for gene

e.g. human blood, kidney, foetal lung, placenta, testes, brain. ovary, pituitary, retina and colon cDNA libraries

Claim 1; Page 486; 633pp; English.

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Gaps

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Indels

Length 605;

Score 17; DB 20; I Pred. No. 1.8e+02; Mismatches

0.6%; Scc. 100.0%; Prev 0; }

Conservative

Similarity

Query Match Best Local S

Matches

14 3 84

31 gttttggtggagacggg 47

Sequence 605 BP; 149 A; 126 C; 194 G; 136 T; 0 other;

therapy.

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                                                                                                                                                                            tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                               polynucleotides encoding human secreted proteins - derived from
                                                                                                                                                                     secreted protein; haematopoiesis regulator;
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     Length 590;
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                     Indels
     DB 20; L
1.8e+02;
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                       Mismatches
    Score 17;
Pred. No.
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Treacy M;
0.6%; Scc.
100.0%; Pre
0;
                                                                                                 V87198 standard; cDNA; 605 BP.
                                                                                                                                                                                                                                                                                    97US-0835913.
                                                                                                                                                                                                                                                                  98WO-US06954
                                      654 aggeoteteageagget 670
                                                                                                                                    27-APR-1999 (first entry)
                                                        29
                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC
                      Conservative
                                                                                                                                                                    Expressed sequence tag;
tissue growth; activin;
                                                                                                                                                                                                                                                                                                                     r, Jacobs K,
Spaulding V,
                                                       75 AGGCCTCTCAGCAGGCT
                                                                                                                                                                                                                                                                                                                                              WPI; 1999-070076/06.
     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                     EST clone BN180.
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                 WO9845435-A2.
                                                                                                                                                                                                                                                                                    10-APR-1997;
                                                                                                                                                                                                                                                                  10-APR-1998;
                                                                                                                                                                                                                                                                                                                     Agostino MJ,
Racie LA, Sp
                                                                                                                                                                                                                                                  15-OCT-1998.
                                                                                                                  V87198;
                                                                                 35
                                                                               RESULT 3
V87198/c
ID V871
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severity of an immune response or to treat cancer. TRAIN-R blocking agents can also be used to reduce the severity or effects of an immunological disease (all claimed).

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Sequence 791 BP; 202 A; 189 C; 165 G; 235 T; 0 other;

Ouery Match

0.6%; Score 17; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0;

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RESULT 37 Z91823

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Gaps

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Length 791; Indels

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The present sequence includes an exon encoding the C-terminus (see W98147) of a soluble form of a novel human cysteine-rich tumour necrosis factor receptor family member termed TRAIN.R. It comparises clone G3156, obtained from a Clontech human adult lung cDNA ilbrary. The encoded 30-amino acid C-terminal peptide is identical to amino acids 121-149 of the composite TRAIN.R protein given in W98146 and to amino acids 121-150 of the C-terminus of murine TRAIN.R short form (secreted protein, see W98144). The soluble protein is expected to inhibit signalling by the full-length TRAIN.R. Human TRAIN.R is expressed at low levels in every tissue and cell line tested thus far, with higher expression detected in heart, prostate, ovary, testis, peripheral blood lymphocytes, thyroid and adrenal gland. Cell death can be induced by administering an agent capable of inhibiting the binding of TRAIN.R to its ligand. A claimed method of treating, or reducing, the amammal comprises administering a mammal comprises administering an immunological disease in a mammal comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "TRAIN-R secreted form C-terminus" 45..790
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                            TRAIN-R; receptor; human; tumour necrosis factor receptor; agonist; antagonist; cancer; immunological disease; therapy;
                                                                                                                                                                                                                                                                                                                               Clone GJ156 encoding TRAIN-R secreted form C-terminus.
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1..350
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                                                                                                                                                               ВР
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                                                                                                                                                               X24979 standard; cDNA; 791
212 GTTTTGGTGGAGACGGG 196
                                                                                                                                                                                                                                                                         (first entry)
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351..790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-229238/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W98147
                                                                                                                                                                                                                                                                                                                                                                                                               agonist; antag
cytostatic; ss
                                                                                                                                                                                                                                                                         05-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1998;
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                                                                                                                                                                                                                     X24979;
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74979/
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This sequence encodes a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunospens or antigens. Immunospens or antigens. Compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or diagnostic aspable of antagonising, inhibiting or interfering with them. Agents, capable of antagonising, inhibiting or interfering with them. Agents, capable of the protein or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in they can be used to treat bacterial pneumonia, which has high rates in they can be used to treat discretize, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
                                                                                                                                                      Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS; bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; immunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Le Page RWF, Wells JM, Hanniffy SB, Hansbro PM;
                                                                                                                     Streptococcus pneumoniae DNA sequence ID33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 47-48; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB02452.
                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-0016336.
                                                                             (first entry)
291823 standard; DNA; 855
                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                    WO200006738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; Y81727
                                                                             02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1999;
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19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                            10-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitis
                                         291823;
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Sequence 855 BP; 235 A; 173 C; 202 G; 245 T; 0 other;

pharmaceutical composition which comprises a TRAIN'R blocking agent, e.g. soluble TRAIN'R. TRAIN'R can be fused to an immunoglobulin to produce a fusion protein which may be targeted to various sites. It can be used in binding assays, and to identify antagonists and agonists. Anti-TRAIN'R antibodies can be used to reduce the

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Pred. No. 1.7e+02; Mismatches 0;

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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COX WI,
                                                                                                                                                                                                                                                                                               967866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                 RESULT
Q67866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                          ö
                       Length 855;
                    0.6%; Score 17; DB 21; Length 85
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obata Y, Old LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Hare M, Obata Y, Old
Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1022 BP; 230 A; 273 C; 302 G; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 67; Page 780; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                               X40199 standard; DNA; 1022 BP.
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97US-0896164.
97US-0061599.
97US-0061765.
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                                                                                                                      97GB-0021697
                                                                                                                                                                        139 gatttggaagagtttca 155
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Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                       Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE-4 encoding gene.
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P-PSDB; Y06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer; ss.
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Tureci O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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10-OCT-1997;
11-OCT-1997;
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28-JAN-1999

x40199;

38

RESULT X40199

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17-JUL-1997 10-OCT-1997 22-JUN-1998

Chen Y,

Length 1022;

Score 17; DB 20;

0.68;

Query Match

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The sequences given in Q67865-66 represent expression cassettes containing the vaccinia H6 promoter and the human MAGE-1 gene which encodes human melanoma-associated antigen MZ2-E, in VCP235 and pMAW037, respectively. These sequences were used in the construction of NYVAC- and ALVAC-based recombinant viruses containing the MAGE-1 gene. MAGE-1 is expressed in primary melanoma tumour cells, melanoma-derived cell innes and certian tumours of non-melanoma origins but not in normal cells except in testis. A first PCR fragment containing the last 18 bp and the initial 24 nucleotides of the MAGE-1 gene was generated and ligated to a second PCR fragment amplified from plasmid pYZ18RMAGEI which contains the initial 546 bp of the MAGE-1 coding sequence. The terminal sequence of MAGE-1 was amplified and a fusion product was generated containing the H6 promoter and the full length MAGE-1 sequence. This construct may be introduced in to the poxvirus derived plasmids,
                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; MAGE-1; melanoma-associated antigen; MZ-E; testis; pTZ18RMAGE1; primary melanoma tumour cell; melanoma derived cell line; tumour; poxvirus; antigenic response; immunological response; pathogen; ss.
                            Gaps
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated recombinant virus used for cancer therapy - DNA encoding cytokine and/or tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52..178
/*tag= b
/note= "Vaccinia H6 promoter"
                                                                                                                                                                                                                                                                  H6/MAGE-1 expression cassette from pMAW037.
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/note= "Flanking sequence"
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"Flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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100.08; PI
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/product= MAGE-1
1010..1084
                                                                                                                                                                       Q67866 standard; DNA; 1084 BP.
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94US-0184009.
                                                           1652 ggtcctgggcaccctgg 1668
                                                                                           203 ggtcctgggcacctgg 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                      22-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..1009
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19-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                     Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; dene therapy; rabies; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4, melanoma associated antigen; carcinoembryonic antigen; immunoisation; antigent; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
ALVAC and NYVAC. The resulting viruses may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                             H6/MAGE-1 expression cassette and flanking regions from pMAW037.
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                                                                                           Query Match 0.6%; Score 17; DB 15; Length 1084; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 0; Indels (
                                                     Sequence 1084 BP; 266 A; 256 C; 280 G; 282 T; 0 other;
                                                                                                                                                                                                                                              Z08442 standard; DNA; 1084 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81US-0334456.
82US-0446824.
84US-0622135.
87US-0090209.
87US-0090711.
87US-0110335.
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90US-0537882.
90US-0537890.
91US-0638080.
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94US-0306259
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91US-0805567
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                                                                                                                                                                                                                                                                                                  19-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HEAL-) HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1984
27-AUG-1987
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14-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                       patient and therefore induces an immunological response. (I) may be used to vaccinate patients against a wide range of diseases and disorders be used to vaccinate patients against a wide range of diseases and disorders be used to vaccinate against diseases such as rabies, influenza and Newcastle Disease. It is particularly useful for immunising against cancers. The poxxirus (I) also provides a means of manipulating lymphocytes and tumour cells for use in cell-based immunotherapeutic modalities for cancer. (I) also have enhanced safety compared to unattenuated viruses (attenuation reduces the virulence of the viruses) and known recombinant poxvirus vaccines. This increased level of safety reduces the possibility of a 'tunaway' infection in the host and reduces the chance of transmission from vaccinated to unvaccinated individuals
                                                                                                                                                                                                                                                                                                                                                                                                         and contamination of the environment. The present sequence represents a H6/MAGE-1 expression cassette and flanking regions from pMAW037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; MAGE-1; melanoma-associated antigen; MZ2-E; testis; pTZ18RWAGE1; primary melanoma tumour cell; melanoma-derived cell line; tumour; poxvirus; antigenic response; immunological response; pathogen; ss.
                                                                                                                                         The present invention describes a recombinant poxvirus (I), comprising exogenous DNA encoding an antigenic determinant of a pathogen which is then expressed in vivo in infected host cells after administration to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                               Recombinant poxviruses comprising exogenous DNA encoding antigenic determinants useful in immunotherapy to immunize against cancers and other diseases such as influenza, Newcastle Disease and rabies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1084 BP; 266 A; 256 C; 280 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 17; DB 20; I
.00.0%; Pred. No. 1.7e+02;
.ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "Vaccinia H6 promoter"
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/note= "Flanking sequence"
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74..200
                                                                                                       Example 16; Fig 20; 163pp; English.
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/product= MAGE-1
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tive 0;
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WPI; 1999-493494/41.
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les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9416716-A.
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promoter
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Matches
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Recombinant poxviruses comprising exogenous DNA encoding antige determinants useful in immunotherapy to immunize against cancer other diseases such as influenza, Newcastle Disease and rabies
                                      87US-0090711.
87US-0110335.
88US-0186054.
88US-0234390.
89US-0320471.
90US-0478179.
82US-0446824.
84US-0622135.
87US-0090209.
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91US-0666056
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2US-0847977
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Matches 17; Conservative
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                                                                                                           FEB-
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ID X2
XX
XX XX
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                                                                                                                                                                                              containing the vaccinia He promoter and the human MAGE-1 gene which encodes human melanoma-associated antigen M22-E, in vCP235 and pMAW037, respectively. These sequences were used in the construction of NYVAC- and ALVAC-based recombinant viruses containing the MAGE-1 gene. MAGE-1 is expressed in primary melanoma tumour cells, melanoma-derived cell lines and certian tumours of non-melanoma origins but not in normal cells except in testis. A first profit ragment containing the last 18 bp and the initial 24 nucleotides of the MAGE-1 gene was generated and the initial 24 nucleotides of the MAGE-1 gene was generated and inject to a second PCA fragment amplified from plasmid pT218RAAGE1 which contains the initial 546 bp of the MAGE-1 coding sequence. The terminal sequence of MAGE-1 was amplified and a fusion product was generated containing the He promoter and the full length MAGE-1 sequence. This construct may be introduced in to the poxylius derived plasmids, ALVAC and NYVAC. The resulting viruses may be used in a composition for inducting an antigenic or immunological response, ie. for immunisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rables; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen; carcinoembryonic antigen; immunulsation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps

    comprises

                                                                                                                                                                                       in Q67865-66 represent expression cassettes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H6/MAGE-1 expression cassette and flanking regions from vCP235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                    Attenuated recombinant virus used for cancer therapy - DNA encoding cytokine and/or tumour associated antigen \,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1094 BP; 269 A; 259 C; 293 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 16; Fig 19; 232pp; English.
                                                                    Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; SCC_
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z08441 standard; DNA; 1094 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0458356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0458356
81US-0334456
 93US-0007115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 ggtcctgggcaccctgg 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0
Matches 17, Conservative
                                         (VIRO-) VIROGENETICS CORP
                                                                    ы
                                                                                                                                                                                       The sequences given
                                                                                           WPI; 1994-263767/32
                                                                                                                                                                                                                                                                                                                                                                                                         against pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Vaccinia virus.
 21-JAN-1993;
19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1995;
24-DEC-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                  Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 42
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ogenous DNA encoding antigenic to immunize against cancers and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unattenuated viruses (attenuation reduces the virulence of the viruses) and known recombinant poxvirus vaccines. This increased level of safety reduces the possibility of a 'runaway' infection in the host and reduce
                                                                                   The present invention describes a recombinant poxvirus (I), comprising exogenous DNA encoding an antigenic determinant of a pathogen which is then expressed in vivo in infected host cells after administration to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             individuals
                                                                                                                                                                                                                                                                 тау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduces the possibility of a 'runaway' infection in the host and reduc
the chance of transmission from vaccinated to unvaccinated individuals
and contamination of the environment. The present sequence represents
                                                                                                                                                                                     patient and therefore induces an immunological response. (I) may be u to vaccinate patients against a wide range of diseases and disorders depending on the type of antigen encoded by the exogenous DNA. (I) may be used to vaccinate against diseases such as rables, influenza and Newcastle Disease. It is particularly useful for immunising against cancers. The poxvirus (I) also provides a means of manipulating modalities for cancer. (I) also have enhanced safety compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions from vCP235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 20; Length 1094; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1094 BP; 269 A; 259 C; 293 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H6/MAGE-1 expression cassette and flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.7; Mismatches
Example 16; Fig 19; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X27353 standard; DNA; 1140 BP.
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osteoclast; thyrus; osteoplorsis; arthritis; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                Human secreted protein gene 43 clone HTADX17
                                                                                                                                                                                                     97US-0051918.
97US-0051919.
97US-0051920.
                                                                                                                                                                                     97US-0058785
97US-0051916
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                                                                                                                                                                    98WO-US13684
11-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                               97US-0052
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                                                                                                                                                                                                                                                                                                                                                   97US-00
                                                                                                                 Homo sapiens
                                                                                                                                  WO9902546-A1
                                                                                                                                                   21-JAN-1999.
                                                                                                                                                                    07-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                    .8-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                              L8-AUG-1997
                                                                                                                                                                                                                                                                                                                                                            8-AUG-1
                                                                                                                                                                                                                                                                                                                                           8-AUG-
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Y, Moore PA; DW, Li Zeng Z; Fischer CL, Kyaw H, Lafleur Ruben SM, Shi Y, Soppet DR, (HUMA-) HUMAN GENOME SCI INC Ebner R, Rosen CA, WPI; 1999-120770/10. P-PSDB; Y02692. Brewer LA, Olsen HS,

97US-0058664

12-SEP-1997

97US-0058660

97US-0055984

97US-0055954 97US-0055964

8-AUG-1997

18-AUG-1997 18-AUG-1997 18-AUG-1997 L2-SEP-1997

97us-0055953

New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 271; 464pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. X27302) for increasing the stability of the fused protein as

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Gaps

; 0

Indels

Mismatches

ö

294 cggtatctcttcaactg 310

δλ

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compared to the human protein only.

The invention relates to 123 novel genes and their fragments (nucleic acid sequences: X27311-X27449; amino acid sequences Y02650-Y02788) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 123 polypucleotides, based on which tissues they are most highly expressed in (see X27311 for described
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening; PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the 3' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5'
                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
                                                                                                                                                                                                                                        Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminus determined
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                       Sequence 1140 BP; 280 A; 312 C; 289 G; 254 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1173 BP; 246 A; 358 C; 310 G; 259 T; 0 other;
                                                                                                                                                                                                                                    0.6%; Score 17; DB 20; L
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.7e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 17; DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 terminus and 1100 nucleotides of the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 28; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus HC-J5 3' region.
                                                                                                                                                                                                                                                                                                                                                                                                                        Q29634 standard; DNA; 1173 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91JP-0191376.
                                                                                                                                                                                                                                                                                                        1802 caaagcctggctccagc 1818
||||||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92EP-0303625
                                                                                                                                                                                                                                                                                                                                        930 caaagcctggctccagc 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.6 Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                        Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMO ) IMMUNO JAPAN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura I, Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-359137/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP510952-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           029634;
                                                                                                                                                           uses).
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
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standard; DNA; 1173

029635 029635

TESULT 129635

(first entry)

16-MAR-1993

910 cggtatctcttcaactg 926

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Forkhead activin signal transducer protein; FAST2; activin signalling; winged-helix/forkhead domain protein; homeobox gene; goosecoid inducer; gsc; transforming growth factor-beta signalling; gsc promoter; signal transduction; transcription factor; wound healing; inflammation; tumour progression; scarring; arthritis; fibrosis; liver fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Forkhead activin signal transducer protein"
//transl_except= (pos: 1183..1185, aa: Cys)
                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of NANB hepatitis virus polynucleotide N-1173-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a forkhead activin signal transducer designated FAST2.
                                                                                                                                                                                                                                                                                                                                                                                                          which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by
                                                                                                                                                                                                                                                                                non-translation region comprising 340 - 341 mols. of nucleotides, nucleotides including region 1,149 and, etc.
                                                                                                                                                                                                                                                                       Antigen related to non-A and non-B hepatitis virus - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 14; Length 1173; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1173 BP; 247 A; 358 C; 309 G; 259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 4..1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Scor
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 29; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z46089 standard; cDNA; 1209 BP
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                                                                                                                                  90JP-0153401
90JP-0304405
                                                                                                   91JP-0196175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 cggtatctcttcaactg 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conventional methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosis; ss.
                                                                                                                                                                                                                    WPI; 1993-199637/25
                                                                                                                                                                                      (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                       P-PSDB; R38285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200004143-A1
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                                 JP05091884-A
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                                                                                                   10-APR-1991;
                                                                                                                                 12-JUN-1990;
08-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2000.
                                                                   16-APR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
246089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the 3' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5' terminus and 1100 nucleotides of the 3' terminus determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                    Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1173 BP; 251 A; 362 C; 304 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; I
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NANB hepatitis virus polynucleotide N-1173-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 1
Pred. No. 1.76
0; Mismatches
                                                                                                                                                                                                                                     PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q43895 standard; cDNA to RNA; 1173 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 2..1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 29; 54pp; English
                                                                                                                                                                                    Hepatitis C virus HC-J6 3' region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                   BP.
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92EP-0303625 91JP-0191376

23-APR-1992; 26-APR-1991;

28-OCT-1992 EP510952-A

Hepatitis C virus

(IMMO) IMMUNO JAPAN INC

Okamoto H;

Nakamura T,

WPI; 1992-359137/44.

non-B hepatitis virus

Non-A,

Key

(first entry):

21-0CT-1993

043895;

SESULT 46 043895

294 cggtatctctcaactg 310

0.7 ð

Matches

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Gaps

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WO9940188-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X87591;
                                                                                    breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X87591
                                                                                                                                                                                                                                                                                                                                                                                                                                           ογ
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                                                                                                                                                                                                           The present sequence encodes a mammalian forkhead activin signal transducer (FAST) protein, designated FAST2. The protein is a winged-helix/forkhead domain protein. The protein is an inducer of the homeobox gene goosecoid (GSC) by transforming growth factor (TGF)-beta or activin signaling. FAST2 binds to a nucleotide sequence in the gsc promoter. The FAST2 protein is useful for modulating signal transduction in a TGF-beta or activin signaling pathway, which involves FAST2 as transcription factor, by modulating the formation of Smad2/Smad4/FAST2 complex. Inhibition of FAST2
                                                                                                                                                                                                                                                                                                                                    binding to its target DNA site inhibits FAST2 specific TGF-beta signaling, which is associated with wound healing inflammation, and tumour progression. Excessive signaling is associated with scarring, arthritis and fibrosis in numerous diseases, including fibrosis of the liver and kidney.
                                                                                                                       New mammalian transcription factor, useful for preventing or treating disorders associated with transforming growth factor beta or activin signaling pathways ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer; bladder cancer; lung cancer; colon cancer; head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 21; Length 1209;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGE-1; CLYIA-MAGE-1-His; fusion protein; tumour; melanoma; breast cancer; bladder cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1209 BP; 247 A; 412 C; 315 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Score 17; ubsect Local Similarity 100.0%; Pred. No. 1.7 Best Local 17. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Streptococcus pneumoniae.
Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                                                   Claim 3; Page 43; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X87593 standard; cDNA; 1338 BP
98CA-2237788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1074 cacatggccccagcatc 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLYTA-MAGE-1-His fusion DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP00660
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98GB-0002543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1999 (first entry)
                            (HSCR-) HSC RES & DEV LP
                                                      Wrana JL, Attisano L;
                                                                                    WPI; 2000-171267/15
                                                                                                  P-PSDB; Y54601.
17-JUL-1998;
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05-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 48
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  okanibalishinda bakkan kanda bahka kanakan
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Gaps
                                                                                                                                                                                                                    of the C-terminal portion of the Streptococcus pneumoniae LYTA protein (CLTAA), the human MAGE-1 tumour-associated antigen and a hexalistidine tail. A vector designed for recombinant expression of the fusion protein in Escherichia coli is provided. The CLYTA moiety provides expression of soluble fusion protein, facilitates affinity purification of the fusion protein, and also acts as a affinity purification of the fusion protein, and also acts as a nimunological fusion partner, e.g. Clyta-MAGE-1-His. These novel fusion proteins provide vaccines for immunotherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and consmall cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus carcinoma.
                                                                  New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of
                                                                                                                                                                                                        This DNA sequence codes for a fusion protein (see Y06592) composed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGE-1; lipoprotein D; LPD-MAGE-1-His; fusion protein; tumour; melanoma; breast cancer; bladder cancer; lung cancer; head and squamous cell carcinoma; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cabezon Silva T,' Cohen J, Slaoui MM, Vinals Bassols C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1338 BP; 335 A; 334 C; 378 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 17; DB 20; I
.00.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 1... tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oesophagus carcinoma; vaccine; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                              Example 9; Page 70-71; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein D-MAGE-1-His fusion DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Haemophilus influenzae.
Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X87591 standard; cDNA; 1341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-EP00660.
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98GB-0002543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 ggtcctgggcaccctgg 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.69
Best Local Similarity 100.0
Matches 17; Conservative
WPI; 1999-494293/41.
P-PSDB; Y06592.
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P-PSDB; Y06590.
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partner such as Deposition of the LPD moiety provides the fusion partner such as LPD. The LPD moiety provides the fusion protein with additional exogenous T-cell epitopes and also increase expression levels in E. coli. The lipid tail ensures optimal presentation of the antigen to antigen-presenting cells. The affinity tag facilitates purification. The novel fusion proteins provide vaccines for immunotherapy of melanomas or other mAAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is shown folded into secondary structure in the specification. It was compared with other sequences available in the literature to design probes specific for SRB. The probes can be used for the rapid identification and quantification of SRB in a sample, e.g. oil-field prodn. waters, water from water treatment facilities, or samples from the gut of ruminant animals.
                                                                                         of Haemophilus influenzae B, the human
                                                        uence codes for a fusion protein (see Y05590) composed protein D (LPD) of Haemophilus influenzae B, the huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assay for sulphate-reducing bacteria - by hybridisation using a labelled oligo-nucleotide probe corresponding to 16S rRNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1341;
                                                                                                              MAGE-1 tumour-associated antigen and a hexahistidine tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRB; Desulphovibro; Desulphotomaculum; ribosomal RNA; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1341 BP; 336 A; 327 C; 351 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16S RNA from ATCC 19858 sulphate-reducing bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Le:
1.7e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Example 6; Page 66; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14450/c
12 Q14450 standard; RNA; 1345 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; ;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 ggtcctgggcaccctgg 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.67
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     and oesophagus carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STAH ) STANDARD OIL CO. (OHIO ) OHIO OIL CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brink DE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                           This DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014450;
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Gaps

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the cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a protein which can release G1 arrest of an animal cell. This sequence was isolated from a human foreskin cDNA library. The protein can be used in the control of the cell
                                                                                                                                                                                                                                             cDNA encoding protein for releasing G1 arrest in an animal cell
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                                                    Length 1345;
                                                                            Indels
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/note= "Given in the specification as 5"
                    Sequence 1345 BP; 331 A; 297 C; 435 G; 249 U; 33 other;
                                                                                                                                                                                                                                                                 Gl arrest; animal cell; human foreskin; cell cycle; ds.
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                                                     DB 12; L
1.7e+02;
thes 0;
                                                     Score 17; DB ]
Pred. No. 1.76
0; Mismatches
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280..1290
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                                              0.6%; SCOL
100.0%; Pre
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                                                                                                                                                                   4/c
T27644 standard; cDNA; 1557 BP.
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                                                                                                                       1274 CGGCTTTCTCAGTTTTG 1258
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Matches 17; Conservative
                                                                            Conservative
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See also Q13729-Q13733.
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P-PSDB; R96248.
                                                                Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                        Query Match
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T98595/c
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                                                                                                                                                        RESULT
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15/c 198595 standard; DNA; 1591 BP

Streptococcus

W09743303-A1

CDS

14-MAY-1997; 14-MAY-1996;

Black MT, 1 Stodola RK;

infections

20-NOV-1997.

DNA encoding 06-NOV-1998

T98595;

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435 GATTTGGAAGAGTTTCA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NOV-1997;
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                                                                                                                                                                                    09-NOV-1998
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                                                                                                                                             V42963;
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V68059
                                                              RESULT
V42963
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on homology with Streptociccus mineral proteins) are GTP-binding proteins ERA homolog, and represents a DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in amammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or I cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extraorallular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                               immunological response; incculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                           pneumoniae protein; genetic immunisation; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence encodes two Streptococcus pneumoniae proteins (based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      implantation of in-dwelling devices or other surgical techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 19; Length 1591; Pred. No. 1.7e+02; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1591 BP; 452 A; 378 C; 313 G; 448 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hodgson JE, Knowles DJC, Nicholas RO;
                                                                                                    GTP-binding proteins ERA homolog.
                                                                                                                                                                                                                                                                                                                                                                     complement (1022..1492)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Pages 129-130; 483pp; English.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers complement (592..1086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; So
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0017670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US07950
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                      /*tag= a
                                                                                                                                                                                                                                                                     pneumoniae.
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P-PSDB; W38537, W38538.
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conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lonetto MA, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1592;
                                                                                                                                                                                                 Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1592 BP; 454 A; 317 C; 376 G; 445 T; 0 other;
                                                                                                                                                    Streptococcus pneumoniae polypeptide coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 19;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 56-57; 181pp; English.
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 573..1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Scc.
100.0%; Pred
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
V42963 standard; DNA; 1592 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . V68059 standard; DNA; 1632 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US21976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0031879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1158 gatttggaagagtttca 1174
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                                                                                                (first entry)
                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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1947 gatttggaagagtttca 1963 ||||||||||||||||||

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Methods have been developed for identifying a compound, which binds to a human or murine D6 protein, an allelic variant or a fragment comprises detecting binding of the test compound to the protein. Also described in the present invention are: (1) a method for identifying a compound capable of treating a disorder characterised by aberrant D6 nucleic acid expression of D6 protein activity; (2) a method for treating a subject having a disorder characterized by aberrant D6 nucleic acid expression comprising administering to the subject a D6 modulator such that treatment of the subject occurs; and (3) methods for identifying a compound that modulates the activity of a Human or murine D6 protein, an allelic variant or a fragment. The methods are useful for identifying compounds capable of treating disorders, especially a respiratory inflammatory disorder, characterized by aberrant D6 nucleic acid expression or D6 protein activity. In particular, the disorder is asthma. D6 modulators are used to treat asthma. The present sequence encodes the murine D6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor-beta superfamily signailing; modulator; Smad2; TGF-beta; detection; FAST-1; MH2 domain; Smad interaction domain; SID; treatment; developmental; disorder; immunological; cancer; diagnosis; ss.
                                                                                                                                                                                                 Identification of D6 G-protein coupled receptor binding compounds and modulators, useful in treatment of asthma
                                                                                           Gutierrez-Ramos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1664 BP; 313 A; 484 C; 436 G; 431 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17; DB 20; I
Pred. No. 1.7e+02;
); Mismatches 0;
                                                                                        Gonzalo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                        Benjamin Nibbs RJ,
                                                                                                                                                                                                                                                                     Claim 2; Fig 2; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V72116 standard; cDNA; 1668 BP
                       (MILL-) MILLENNIUM PHARM INC. (CRCT-) CRC TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US10983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2212 tgctgaaccacttcagc 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse FAST-1 coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                  WPI; 1999-562123/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-059773/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitman M;
                                                                                                                                                            P-PSDB; Y41682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9853830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1998
                                                                                        Graham GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V72116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 56
V72116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                          polypeptide; HHPDZ65; stroke; pain; epilepsy; therapy; disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide of the invention. HHPDZ65 is useful for the treatment of stroke, pain, epilepsy, neurodegenerative diseases and others. The DNAs and proteins are useful in a method for screening to identify compounds which stimulate or inhibit the function of the HHPDZ65 proteins. The polypeptides are useful in a process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the HHPDZ65 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHPD265 polypeptide(s), their corresponding DNA, antibodies, agonists and antagonists - are useful in the treatment of stroke, pain, epilepsy and neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1632;
Neurodegenerative polypeptide HHPDZ65var coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the HHPDZ65var neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1632 BP; 312 A; 529 C; 497 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D6; G proteIn-coupled heptahelical receptor; diagnosis respiratory inflammatory disorder; identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Topp S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 17; DB 19; 300.0%; Pred. No. 1.7e+02; ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Harrison DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine D6 encoding cDNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Page 16; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0%;
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                             Doe TR,
                                                                                                                                                                                                                                                                                        98GB-0003566.
97GB-0008936.
97EP-0310289.
                                                                                                                                                                                                                                           98EP-0302912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579 cacggtccccaggagg 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z25023 standard; cDNA; 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Davis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-559436/48.
P-PSDB; W80318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                          Neurodegenerative
neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09947697-A1.
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                     19-FEB-1998;
01-MAY-1997;
18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1998;
                                                                                                                                                                                                                                           15-APR-1998;
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                                                                                                                                                     EP875570-A2
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                                                                                                                                                                                                 04-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                             Bingham S,
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Mus sp.

SAN SAN CARA

225023;

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HHPDZ65 p agonists

Claim

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Gaps

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Indels

Length 1664;

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Modulating TGF-beta superfamily signalling - comprises use of compounds identified in assays with Smad2, FAST-1 and Smad3, used develop products for treating, e.g. developmental disorders
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Example XII; Page 70; 107pp; English

a method to detect a compound capable of modulating transforming growth factor-beta (TGT-beta) superfamily signalling. The invention describes accomplex which forms between FAST-1 and Smad2 and this complex is specifically induced by signals generated by a TGF-beta superfamily member. A domain of FAST-1 directly interacts with Smad2 and this molecules, namely, the MH2 domains of the two interacting molecules, namely, the MH2 domain of Smad2 and the Smad interacting for the detection and treatment of conditions involving abnormal TGF-beta superfamily signalling. They can be used to treat e.g. developmental disorders, immunological disorders and cancer. The products can also be This sequence encodes a mouse FAST-1 protein which is used in used for detection and diagnosis.

Sequence 1668 BP; 368 A; 517 C; 432 G; 351 T; 0 other;

ö Gaps ö 0.6%; Score 17; DB 20; Length 1668; 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 17; Conservative Query Match

1074 cacatggccccagcatc 1090

57

V69719 standard; cDNA; 1691 BP

V69719;

01-MAR-1999 (first entry)

Tumour rejection antigen precursor MAGE-Al cDNA.

OND STRUKEN SET

MAGE-A1; human; tumour rejection antigen precursor; TRAP; therapy; diagnosis; ss.

Homo sapiens

Location/Qualifiers 204..1133 /*tmg= a

WO9849184-A1.

05-NOV-1998

98WO-US08493. 24-APR-1998;

(LUDW-) LUDWIG INST CANCER RES 97US-0845528 25-APR-1997;

De Smet C, Lucas Boon-Falleur T,

WPI; 1999-024041/02. P-PSDB; W81548.

RECEIVE

Tumour rejection antigen precursors – used for determining presence of cytolytic T cells specific for complexes of a human leukocyte antigen

Disclosure; Page 46-47; 84pp; English.

Sequence 1702 BP; 371 A; 517 C; 476 G; 338 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. Z52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in Y73814-Y74252.
precursor (TRAP) MAGE-Al cDNA, which encodes a 309-amino acid precursor (TRAP) MAGE-Al cDNA, which encodes a 309-amino acid polypeptide (see W8154B). MAGE-Al cDNA shows homology to novel human MAGE-CI cDNA (see V65720), especially in exons 2 and 3.

The open reading frame of MACE-CI, however, is about 2 kb longer than that of MAGE-Al, most of the difference being accounted for by a large repetitive sequence. MAGE-CI (see W81546) is a novel member of the MAGE family that may be recognised by cytotoxic rells, leading to lysis of the tumour cells which express it. It is expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The invention provides MACE-CI and MACE-CI and control of the difference of cytolytic I cells specific method for determining the presence of cytolytic I cells specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilarsky C,
                                                                                                                                                                                                                                                                                                         Length 1691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate tumor cDNA library derived EST fragment #19.
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                       Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 other;
                                                                                                                                                                                                                           for complexes of a human leukocyte antigen (HLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmitt A,
                                                                                                                                                                                                                                                                                                         Score 17; DB 20; 1
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal A, Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 197-198; 502pp; German.
                                                                                                                                                                                                                                                                                              0.6%; Scur-
100.0%; Pre-
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-621386/54.
P-PSDB; Y73868, Y73869, Y73870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98DE-1020190.
                                                                                                                                                                                                                                                                                                                                                                            98DE-1020190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252876 standard; cDNA; 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19820190-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 58
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The present sequence encodes human cell division regulator (HCDR) 1. HCDR proteins are active in interphase, and are used for the treatment or prevention of inflammation and disorders associated with cell proliferation and apoptosis. HCDR may be administered to a patient having a disorder associated with an increase in apoptosis,
                                                                                                                                                                                                                                                                Human cell division regulator; HCDR; interphase; inflammation; cell prolliferation; apoptosis; neurodeficiency; neurodegenerative disease; aplastic anaemia; isohaemic injury; liver damage; viral infection; hepatitis B; hepatitis C; ss.
                                                                                                                                                                                                                            DNA encoding human cell division regulator (HCDR) 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell division regulators active in interphase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1A-E; 59pp; English.
                1565 agggagtggcagaggga 1581
                                                                                                             X85940 standard; DNA; 1816
                                                                                                                                                                                       13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-429499/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; Y23782.
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1997;
01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     US5928899-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            27 - JUL - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandman O,
                                                                                                                                                 X85940;
                                                                      9
                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                          x85940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA encodes a human beta(1 -> 4)·N·acetylglucosaminyl-transferase (GnT-IV)b enzyme. The invention provides bovine and human GnT-IV enzymes that can be used for converting sugar chain subunits having one structure to another structure. Vectors containing the DNA sequences encoding these enzymes can be used to transform host cells for the production of the GnT-IV enzymes. The enzymes are useful in the production of branched oligosaccharides and polysaccharides which are difficult of access by other methods. They are also useful in the production of drugs, reagents and foods and in modifying the properties of biopolymers containing sugar chains. The enzyme may also be used for the preparation of glycoproteins
                                                                                                                                                                                                                                                                                                                                                                             Beta(1 -> 4)-N-acetylglucosaminyl-transferase; GnT-IV; bovine; human;
enzyme; sugar chain subunit; branched oligosaccharide; polysaccharide;
drug; reagent; food; biopolymer; glycoprotein; erythropoietin; ss.
                                                                                                                                                                                                                                                                                                                                           Beta(1 -> 4)-N-acetylglucosaminyl-transferase (GnT-IV)b encoding cDNA.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant beta(1-4)N-acety1:glucosaminy1:transferase - allows production of difficultly accessible branched poly:saccharides food and drug use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1724;
              Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida A;
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1724 BP; 353 A; 553 C; 501 G; 317 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17; DB 19; I larity 100.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 0;
        Score 17; DB 20;
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taniguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
43..1689
/*tag= a
/product= "GnT-IVb enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Pages 70-74; 112pp; Japanese.
0.6%; Scc.
100.0%; Pre
0; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeuchi M,
                                                                                                                                                                                                                        V38385 standard; cDNA; 1724 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-JP04546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0161462
                                                                                                                       1112 agggagtggcagaggga 1128
                                                                                    1341 agggagtggcagaggga 1357
|||||||||||||||||
                                                                                                                                                                                                                                                                                                    (first entry)
        Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as erythropoietin.
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oguri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-348516/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W63559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9826053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1997;
12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                    24-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minowa M,
                                                                                                                                                                                                                                                              V38385;
                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                   RESULT
V38385
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Shah P;

Lal P,

Corley NC, Hillman JL,

98US-0165234. 97US-0951148. 98US-0165234.

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; HCDR-1; HCDR-2; HCDR-3; human cell division regulator; apoptosis; inflammation; cell proliferation disorder; adenocarcinoma; AIDS; ss.
                                                                                                                                                    Gaps
such a disorder may be e.g. neurodeficiency, a neurodegenerative disease, aplastic anaemia, an ischaemic injury, liver damage, or viral infection such as hepatitis B or C.
                                                                                                                                                  ;
0
                                                                                                                 0.6%; Score 17; DB 20; Length 1816;
                                                                                                                                                  0; . Indels
                                                               Sequence 1816 BP; 494 A; 473 C; 494 G; 355 T; 0 other;
                                                                                                                                  1.7e+02;
                                                                                                                                 Pred. No. 1.7
Mismatches
                                                                                                                   100.0%; Pre-
                                                                                                                                                                                                                                                                                                  X01577 standard; DNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                                                    Human HCDR-1 coding sequence.
                                                                                                                                                                                  804 ggaaacttcttggtgct 820
                                                                                                                                                                                                     04-MAY-1999 (first entry)
                                                                                                                                                    Conservative
                                                                                                                                 Best Local Similarity
Matches 17; Conserv
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                 x01577;
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Gaps

Indels 0;

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The present sequence is the coding sequence of human TRAF four associated factor TRAF2. The gene was discovered by screening a human placenta cDNA library using a two-hybrid system. The protein associates with the TRAF domain located at the carboxyl-terminal of TNF seceptor associated factor 4 (TRAF4), which is believed to be an oncoprotein. Antiboddes that bind to TNF four associated factors (TRAFs) may be used to treat or diagnose tumours (e.g. breast cancer) when labelled with an isotope or an appropriate drug, precursor or enzyme. Antagonists, agonists, and antisense sequences of TRAFs may be used to treat cancers. TRAF proteins, antibodies that recognise them and DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitrite reductase; transgenic crop; transgenic tree; detoxification;
                                                                                                                                                                                                                                                     Novel tumour necrosis factor receptor associated factor 4 associate factors useful for developing cancer screens, and treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1906 BP; 655 A; 320 C; 372 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or them may be useful as tools for cancer research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 17; DB 21; I larity 100.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 0;
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                                                                                                      (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T09084 standard; cDNA to mRNA; 2160 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= poly_A_site
                                                                                                                                                                                                                                                                                                                    Claim 4; Page 47-50; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Populus nigra L. var italica
                 98CA-2245340
                                                            98CA-2245340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2796 gtttttaaagaagtctt 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 GITITIAAAGAAGICIT 566
                                                                                                                                          Toji.S, Tamai K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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2146..2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                  WPI; 2000-351124/31
P-PSDB; Y94209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                 19-AUG-1998;
                                                            19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP07236486-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1996
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                                                                                                                                            Yano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T09084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes the human cell division regulator-1 (HCDR-1) protein of the invention. Polynucleotides complementary to the HCDR-1 coding sequence can be used as probes to detect the DNA in a sample. The polynucleotide sequences encoding HCDR may be used to prevent/treat inflammation and disorders associated with cell proliferation and apoptosis and in assays that detect activation of cancers. Polynucleotides encoding HCDR may be used for the diagnosis of conditions associated with expression of HCDR, including disorders associated with cell proliferation/apoptosis e.g. adenocarcinoma and AIDS. The polynucleotides may also be used in Southern or Northern analysis, dot blot, or other membrane based technologies; in PCR technologies; or in dipstick, pin, or ELISA assays or microarrays utilising fluids or tissues from patient biopsies to detect altered HCDR expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFAF2; TRAF four associated factor 2; tumour formation; breast cancer; TRAF4; TNF receptor associated factor; tumour diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human cell division regulators (HCDR) - useful for diagnosing, preventing and treating inflammation and disorders associated with cell proliferation and apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 20; Length 1818;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TRAF four associated factor TFAF2 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1818 BP; 494 A; 473 C; 494 G; 355 T; 2 other;
                                                                                                                                                                                                                                                                           Shah P;
                                                                                                                                                                                                                                                                           Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A15550 standard; cDNA to mRNA; 1906 BP.
                                                                                                                                                                                                                                                                           Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/product= TFAF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 1; 59pp; English
                                                                                                                                              97US-0951148.
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                                                                                                                                                                                       97US-0951148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                           Bandman O, Corley NC,
                                                                                                                                                                                                                                                                                                                 WPI; 1999-166646/14.
P-PSDB; W73971.
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                    Homo sapiens,
                                                                                                                                            15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                            US5871973-A
                                                                                                      16-FEB-1999
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A15550;

Key

ESULT 62 (15550/c 7 A15550

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Gaps

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Length 1906; Indels Baughn MR;

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The present cDNA sequence encodes human epidermal protein-6 (HEPI). The cDNA clone is derived from PTHYNOT03 library which was constructed using fema isolated from left parathyroid tissue of a 69-year-old caucasian female during a partial parathyroidectomy. Recombinant, vectors comprising HEPI cDNA are introduced into host cells for protein expression. The HEPI proteins are useful for the treatment of epithelial disorders, including dyshidroic cozema and scabies, cell proliferative disorders including actinic keratosis and arteriosclerosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour rejection antigen; vaccine; cancer; E antigen precursor gene; ss.
                                                                                                            New human epidermal proteins (HEPI-1) to (HEPI-6) useful for the diagnosis, treatment and prevention of epithelial, cell proliferative, and autoimmune inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                         proteins are useful for treating disorders associated
                                                                                                                                                                                                                                                                                                                                      autoimmune/inflammatory disorders like acquired immune deficiency syndrome (AIDS) and Addison's disease. Pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Length 2284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumour rejection antigen is useful as a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lurquin C, Traversari C; P, Van Pel A;
             Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2284 BP; 452 A; 775 C; 534 G; 523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 21; I
Pred. No. 1.7e+02;
); Mismatches 0;
             Guegler KJ,
                                                                                                                                                                          Claim 7; Page 78-79; 82pp; English.
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Van Den Eynde B, Van Der Bruggen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
             Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                          with altered HEPI expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0705702.
91US-0728838.
91US-0764365.
91US-0807043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2262 CAGGAAGGGCTGAGAT 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1881 caggaagggctgagat 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X84103 standard; DNA; 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E antigen precursor gene.
                                                            2000-195295/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-418294/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancerous diseases
             Lal P,
                                                                                                                                                                                                                                                                                                                                                                           comprising HEP1
                                                                             P-PSDB; Y44989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5925729-A.
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09-JUL-1991,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1991
12-DEC-1991
               XΙ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x84103;
               Tang YI
Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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X84103
ID X84
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                                                                                                                                                                                                                                                     The gene encodes a nitrite reductase gene isolated from Populus nigra. The gene is useful in generation of street trees with a high power for clarfiying NO2, an atmospheric pollutant. The gene can also be used in transgenic plants, esp. crops, bred to contain less nitrosamines (a carcinogenic substance present in food).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dyshidrotic eczema; cell proliferative disorder; actinic keratosis; arteriosclerosis; autochumune disorder; inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; antiHIV; dermatological; anitarterlosclerotic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                        Nitrite reductase gene from Populus nigra - useful for breeding
trees to remove nitrogen di:oxide from the atmosphere or for crops
which produce fewer carcinogenic nitrosamine(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epidermal protein-6; HEPI; epithelial disorder; scabies;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 2160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mature human epidermal protein-6"
                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 16; Length 21
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 2160 BP; 660 A; 388 C; 570 G; 542 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human epidermal protein-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cocation/Qualifiers
                                                                                                                                                                                                                          Claim 1; Page 5-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pr
ative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12/c
250582 standard; cDNA; 2284 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human epidermal protein-6 cDNA
                                             94JP-0032359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0155203.
             94JP-0032359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcttgccaagtatcttg 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 GCTTGCCAAGTATCTTG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product=
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148..1636
/*tag= c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c./product=
                                                                             (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                            WPI; 1995-347454/45.
P-PSDB; R87973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200006727-A2
             02-MAR-1994;
                                             02-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1998;
07-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1711
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Gaps

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0; Indels

conditions

888888888°

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Gaps

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Indels

Length 2419;

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072476 encodes tumour rejection antigen E, another sequence concodes melanoma antigen-3 (MAGE-3) a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytolytic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human
new family of genes refered to as melanoma antigens (MAGE) (see also Q32352-69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour rejection antigen E; melanoma antigen-3; MAGE-3; cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17; DB 15; Length 2419;
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumour rejection antigen precursor MAGE3 - useful in treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                     Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                                                                                      0.6%; Score 17; DB 13;
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaugler B, Van DEN EYNDE B,
                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour rejection antigen E encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 58; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0°,
100.0%; Pie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leucocyte antigen (esp. HLA-A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T05086 standard; DNA; 2419 BP.
                                                                                                                                                                                                                                                                                                                                                                                               Q72476 standard; DNA; 2419 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US02877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0037230
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                                                                                                                                                                                                                                                                                     739 ggtcctgggcaccctgg 755
                                                                                                                                                      Ouery Match 0.6%
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 0.65
Best Local Similarity 100.9
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-333192/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boon-falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09423031-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                       972476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 68
T05086 .
ID T05086
                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                        072476
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                                                                                                                                                                                                                                            δλ
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                                                                                       This sequence represents the E antigen precursor gene. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stable, antigen; E; D; F; A; human; melanoma; cell line; MZ2-MEL; cytolytic T cell; MEL3.1; open reading frame; homology; MAGE;
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                   Length 2418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Traversari C;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                    Sequence 2418 BP; 562 A; 582 C; 675 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                Score 17; DB 20; I
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boon T, Chomez P, De Plaen E, Lurquin C, Tra
Van Den Eynde B, Van Der Bruggen P, Van Pel A;
                                             Example 20; Column 15-18; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 69-70; 142pp; English.
                                                                                                                                                                                                                                                 0.6%; Scc.
100.0%; Pre
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q32351 standard; DNA; 2419 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-US04354.;
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91US-0728838.
91US-0764364.
91US-0807043.
                                                                                                                                                                                                                                                                                                                                                      1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                            738 ggtcctgggcaccctgg 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanoma antigen; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-415460/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen E gene.
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22-APR-1993

032351;

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TIDSE.

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Homo sapiens

WO9220356-A. 26-NOV-1992 22-MAY-1992; 23-MAY-1991; 09-JUL-1991; 23-SEP-1991; 12-DEC-1991;

Van DER BRUGGEN P;

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Gaps

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Indels

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072472 is the tumour rejection antigen E precursor gene, another gene Q72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
                                                                                                                                                                                                                                                                                     This sequence represents the antigen E coding sequence. The invention relates to a tumour rejection antigen sequence useful as a tumour rejection antigen for vaccination against
                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 2419;
1.7e+02;
                                                                                                                                                                                                          New tumour rejection antigen is useful as a vaccine against
                                                                                                                           Lurquin C, Traversari
P, Van Pel A;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour rejection antigen E precursor gene DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumour rejection antigen precursor MAGE3 treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 2
Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van DEN EYNDE
                                                                                                                                                                                                                                                         Disclosure; Column 37-40; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 20; Page 28; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Boon I, Chomez P, De Plaen E,
Van Den Eynde B, Van Der Bruggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q72472 standard; DNA; 2420 BP
94US-0142368.
91US-0705702.
91US-0728838.
91US-0764365.
91US-0807043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US02877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-333192/41.
                                                                                                                                                                           WPI; 1999-418294/35
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                           cancerous diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boon-falleur T,
 02-MAY-1994;
23-MAY-1991;
09-JUL-1991;
23-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-0CT-1994
                                                                                                                                                                                                                                                                                                                                      conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          072472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q72472
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A gene sequence (T05086) hybridizes with a 2.4 kb fragment from human melanoma cell line M22-MEL but not with E- antigen loss variants of M22-MEL. This E precursor antigen gene sequence was obtd. from a cosmid derived from DNA of the E+ subclone M22-MEL 43.
                                                                                                            Melanoma; MZ2-MEL; tumour rejection antigen; cancer; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determn. of cancerous condition(s) - using a nucleic acid as a primer to determine expression of a MAGE tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Pred. No. 1.7e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour rejection antigen; vaccine; cancer; antigen E; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2419 BP; 560 A; 581 C; 677 G; 601 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 20; Page 69-70; 121pp; English.
                                                                             M22-MEL antigen E precursor gene
                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                      94US-0346774.
94US-0204727.
94US-0209172.
94US-0299849.
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                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen E coding sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-320586/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                             Homo sapiens
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                                               26-FEB-1996
                                                                                                                                                                                                                                        23-FEB-1995;
                                                                                                                                                                                                                                                                                                   10-MAR-1994;
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01-MAR-1994;
                                                                                                                                                                                                         08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
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Gaps

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Indels

Van DER BRUGGEN P;

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agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytolytic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours; HLA-restricted cytotoxic T-lymphocyte activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used to produce the C-terminal MAGE-1 peptides described in R70915 to R70969. These peptides are useful for defining epitopes that engender a HLA-restricted cytotoxic lymphocyte activity against MAGE-1 antigens. Compans. containing these peptides can be administered, as a vaccine to patients susceptable to MAGE
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                                                                                                                      Length 2420;
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human melanoma antigen, MAGE-1, peptide(s) - useful for
stimulating immune response against melanoma
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                                                                          Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 other;
                                                                                                                      0.6%; Score 17; DB 15;
100.0%; Pred. No. 1.7e+02;
iive 0; Mismatches 0;
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626..1555
/*tag= a
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                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                  93US-0103623
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                                                                                                                                                                                                                                                                                         Q85435 standard; DNA; 2420
                                                                                                                                                                                                                                                                                                                                                   09-OCT-1995 (first entry)
                                                                                                                      Query Match 0.69
Best Local Similarity 100.0
Matches 17; Conservative
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935435
10 085435
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Gaps

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1652 ggtcctgggcaccctgg 1668 ||||||||||||||||||

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                         Human secreted protein gene 85 clone HSDFV29.
                                                              V59595 standard; DNA; 2503 BP.
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970S-0043672.
970S-0043674.
970S-0047492.
970S-0047500.
970S-0047501.
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970S-0047582.
970S-0047583.
970S-0047584.
970S-0047585.
970S-0047585.
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97US-0043669.
97US-0043670.
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970S-0047588.
970S-0047589.
970S-0047590.
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97US-0040163
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97US-0043313
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97US-0043576
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97US-0047593
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97US-0047596
739 ggtcctggggcaccctgg 755
                                                                                                                 06-JAN-1999 (first entry)
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                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                           WO9839448-A2
                                                                                                                                                                                                                                                                                                                                                           06-MAR-1998;
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23-MAY-1997
                                                                                        V59595;
                                      RESULT
                                                  V59595
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New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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le AM, Fischer CL, Florence KA, Greene JM, Hu JS;
eur DW, Li Y; Moore PA, Ni J, Olsen HS, Rosen CA;
i Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 316-317; 721pp; English.
970S-0047597.
970S-0047598
970S-0047599.
970S-0047600.
970S-0047601.
970S-0047613.
970S-0047613.
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97US-01
97US-00
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Lafleur DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W74815
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Kyaw H,
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This sequence represents a nucleic acid molecule designated Gene 85 from the human cDNA clone HSDFY29 (deposited as clone ATCC 209076) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. V59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V59511-V59812; amino acid sequences W74731-W75025) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polyneclecities. Specific uses are described for reach of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V5911 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling BSTs (expressed sequence tags) from a particular tissue type before comparison of
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Ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents ^{-1}
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 19; Length 2503;
Pred. No. 1.7e+02;
D; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 2503 BP; 561 A; 705 C; 658 G; 568 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endometrium tumour cDNA derived EST 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (META-) METAGEN GES GENOMFORSCHUNG MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 253; 444pp; German.
                                                                                                                                                                                                                                                                                                                                                                0.6%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z42096 standard; cDNA; 2646 BP.
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ses 17; Conservative
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                                                                                                                                                                                                                                                                                uses).
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242096
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Endress GA;

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expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. Z41981-Z42121 represent EST fragments derived from a human endometrium tumour cDNA library which encode the protein sequences represented in Y59941-Y60328.
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Sequence 2646 BP; 787 A; 502 C; 546 G; 811 T; 0 other;

ö Gaps ö Length 2646; Indels Score 17; DB 20; I Pred. No. 1.7e+02; 0; Mismatches 0; 0.6%; Sur-100.0%; Pre 0; / Conservative Query Match Best Local Similarity Matches 17; Conserv

1717 agccccagcagagaaa 1733

74 TESULT .. 58056

V68056 standard; DNA; 2711 BP

V68056;

02-FEB-1999

Neurodegenerative polypeptide HHPDZ65 coding sequence.

Neurodegenerative polypeptide; HHPDZ65; stroke; pain; epilepsy; therapy; neurodegenerative disease; ss. NUMBER ANNA KONGROUNDE ANNA MARKET ANNA COLOCOCOCO

Homo sapiens

EP875570-A2

04-NOV-1998

98EP-0302912 15-APR-1998;

98GB-0003566. 97GB-0008936. 97EP-0310289. 19-FEB-1998; 01-MAY-1997; 18-DEC-1997; (SMIK) SMITHKLINE BEECHAM PLC

Harrison DC, Doe TR, Davis J, Bingham S,

ŝ Topp

WPI; 1998-559436/48. P-PSDB; W80315.

HHPD265 polypeptide(s), their corresponding DNA, antibodies, agonists and antagonists - are useful in the treatment of stroke, pain, epilepsy and neurodegenerative diseases

Claim 7; Page 14; 31pp; English.

invention. HHPDZ65 is useful for the treatment of stroke, pain, epilepsy, neurodegenerative diseases and others. The DNAs and proteins are useful in a method for screening to identify compounds which stimulate or inhibit the function of the HHPDZ65 proteins. The polypeptides are useful in a process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the HHPDZ65 polypeptides. This sequence encodes the HHPDZ65 neurodegenerative polypeptide of the

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0.6%; Score 17; DB 9; Length 2971; 00.0%; Pred. No. 1.7e+02;

Mismatches

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1781 CCATATCGCAGGCACCC 1765

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112 ccátatcgcaggcaccc 128

100.08;

Ouery Match Best Local Similarity 100. Matches 17: "Conservative

3000 BP

Q13115 standard; cDNA;

RESULT 76 Q13115

013115;

22-OCT-1991 (first entry)

Sequence 2711 BP; 559 A; 820 C; 852 G; 478 T; 2 other;

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Gaps
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Query Match 0.6%; Score 17; DB 19; Length 2711; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 0; Indels 0
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Recombinant DNA contg a consensus sequence common to genes that are repressible by oxygen and inducible by formate under anaerobic conditions and the fdhF promoter used as a simple expression system for foreign genes. Expression does not require temp shifts or addition of inducers. (Formate is produced naturally by microorganisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA contg consensus sequence and specific promoter providing foreign gene repression under anaerobic conditions
                                                                                                                                                                       repression/expression of foreign genes by oxygen/formate;
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                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                            /*tag= a
/product=fdhF
737..740
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            late, anaerobic growth phase)
See also N81165.
                                                                  N81166/c
ID N81166 standard; DNA; 2971 BP.
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2624 cacggtcccccaggagg 2640
                     1879 cacggtcccccaggagg 1895
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87DE-3735381
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                                                                                                                                                                                                                                  749..2896
                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1987;
09-OCT-1987;
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                                                                                                                             29-OCT-1990
                                                                                                                                                                                                                                                                                                                            05-OCT-1988
                                                                                                                                                                                                                                                                                                     EP285152-A.
                                                                                                                                                   fdhF gene
                                                                                                                                                                                              synthetic
                                                                                                      N81166;
                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                   RBS
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This polynucleotide comprises clone pA1276 that codes for human T-cell surface antigen CD97 (see W48756). It was isolated from a T-cell library enriched for mitogen-induced genes. The invention relates to the previously unrecognised alpha subunit of CD97 that acts in the establishment and maintenance of inflammation. Soluble CD97 acts as an adhesion factor for endothelial cells and smooth muscle cells, implicating it as a modulator of atherosclerosis. CD97 alpha also acts as a motility factor to cells bearing the alpha(v)beta-3 receptor, indicative of a role in angiogenesis. Soluble CD97 alphal, alpha2, and alpha3 subunits (having different combinations of EGF repeats) all originate as a proprotein with the beta subunit (see W48756). Host cells transfected with a nucleic acide encoding a CD97 alpha subunits are claimed. CD97 alpha subunit polypeptides, nucleic acids, antibodies and antagonists (e.g. CD97 subunit antisense nucleic acids) are used in claimed complementations for indiamed to methods for: determining the degree of inflammation and are site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atheroslerosis; and treating or inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 7-transmembrane receptor; lectomedin; lectin-binding; mucin; olfactomedin; cellular adhesion; atherosclerosis; gene therapy; vascular disease; CD97; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibit soluble CD97 alpha subunit
logenesis associated with chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3156;
                                                                                                                                                                                                                                                                                                                                                                           New soluble CD97 alpha subunit isoform(s) - used to develop products for the detection and treatment of inflammation, atherosclerosis and angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3156 BP; 652 A; 973 C; 860 G; 671 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 17; DB 19; I
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compounds that inhibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CD97 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z27969 standard; DNA; 3156 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD97 associated inflammation.
                                                                                                                                                                     97WO-US19772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1336 ccaggagggagtggcag 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2683 ccaggagggagtggcag 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2000, (first entry)
49..99
/*tag= b
100..2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting
                                                            /*tag=
                                                                                                                                                                                                                                                                                                                  WPI; 1998-261492/23.
P-PSDB; W48756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                                     24-OCT-1997;
                                                                                             WO9817796-A2
 sig_peptide
                                                                                                                                  30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying
                                         nat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z27969;
                                                                                                                                                                                                                                                                                   Kelly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
Z27969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Overlapping clones which make up this sequence were isolated from a mouse Peripheral Blood Lymphocyte lambda gt10 cDNA library. The protein encoded by this sequence is purified and can mediate the cytolytic activity of mammalian cells. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell surface antigen; CD97; human; inflammation; angiogenesis; atherosclerosis; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a natural killer cell receptor – used to develop prods. for the immuno-detection and immuno-therapy of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3000;
                                                          NK; cytotoxic drugs; tumour cell; immunotherapy; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 12; Length 30
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3000 BP; 997 A; 661 C; 716 G; 626 T; 0 other;
                       Encodes partial murine Natural Killer receptor.
                                                                                                                                                                                                                            /*tag= b
/product= murine NK receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
49..2556
/*tag= a
                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                    /*tag= a
/note= "partial"
22..2946
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell surface antigen CD97 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V18471 standard; cDNA; 3156 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                900S-0535206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0143578
                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) NAT INST OF HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ortaldo J, Young H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-245694/33.
P-PSDB; R13320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also Q13114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           08-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1990;
                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1998
                                                                                                                                                                                                                                                                                 US7535206-A
                                                                                                                                                  sig_peptide
                                                                                                                                                                                                           mat_peptide
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Gaps

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V18471;

Key

: SULT 77

2 2

118471

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Overexpression of nitrate reductase (NR) can stimulate the early development of plants, shortening the duration of the vegetative phase and causing earlier germination, flowering and ripening by about two weeks. Overexpression of NR can also cause the level of nitrate stored in a plant to be reduced, reducing risks to health and also possibly improving organoleptic qualities. The NR gene was tunnfroduced into plants by transforming a strain of Agrobacterium tunnefaciens with a plasmid and using it to infect the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus protein; chordin; dorsal tissue; neural tissue; vertebrate; endodermal differentiation; treatment; neurodegenerative disease; nerve cell; transforming growth factor; TGF; secreted protein; ss.
                                                                                                                                                                                                                                                                                             Inducing over-expression of nitrate reductase in plants - esp. by incorporation of foreign gene, for stimulating early development and reducing nitrate accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 17; DB 14; Length 34
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3457 BP; 1014 A; 700 C; 752 G; 991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "hydrophobic signal peptide"
354..3179
                                                                                                                                                                          Chupeau Y, Dorlhac F, Morot-gaudry J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "putative secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus frog protein "chordin" encoding cDNA.
                                                                                                                                        (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Figure 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T93499 standard; cDNA; 3796 BP.
                                                        93WO-FR00222.
                                                                                                92FR-0002658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   909 gaaggaagagatttt 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 GAAGGAAGAGATTTT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
hes 17; Conservative
                                                                                                                                                                                                                                       WPI; 1993-303468/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis.
                                                                                                                                                                                                                                                          P-PSDB; R41757
                                                        05-MAR-1993;
                                                                                                05-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5679783-A.
                16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1997
                                                                                                                                                                              Caboche M,
Vincentz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T93499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T93499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides purified and isolated human 7-transmembrane receptor lectomedin polypeptide or its fragments. The lectomedin polypeptide or its fragments. The lectomedin like and mucin-like domains. The polypeptide can be produced by standard recombinant methodology. The polypeptide is involved in cellular adhesion and cytoplasmic metabolic pathways that are modulated by extracellular signaling. Specific binding to lectomedin-lexpressed on smooth muscle cells may be required for proliferation of these cells in atherosclerosis. The polypeptide is used to raise specific antibodies, and to identify specific binding agents that modulate (increase or decrease) its activity. The lectomedin nucleic acids are used as source of probes and primers, and of therapputic antisense, ribozyme or triplexforming agents and in gene therapy to restore deficient lectomedin activity. Specific binding agents of lectomedin are are used for treating diseases that involve lectomedin activity, e.g. vascular diseases such as atherosclerosis. The present sequence represents the DNA encoding the human CD97 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                         New human lectomedin receptor polypeptide, used to identify specific binding partners for treating e.g. vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrate reductase; germination; flowering; ripening; development; growth stimulation; Agrobacterium tumefaciens; nitrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 17; DB 20; Length 3156;
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3156 BP; 651 A; 974 C; 860 G; 671 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a //product= Nitrate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 106-110; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrate reductase Nia2 gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
144..2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :8/c
Q48468 standard; cDNA; 3457 BP.
                                                                                                                     99WO-US04676.
                                                                                                                                                           98US-0076782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                               WPI; 1999-571596/48
                                                                                                                                                                                                   (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                      P-PSDB; Y41090.
Homo sapiens
                                                                                                                                                           04-MAR-1998;
                                                                                                                   04-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana sp
                                       W09945111-A1
                                                                                                                                                                                                                                           Hayflick JS;
                                                                             10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9318154-A.
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048468;

ONDERSE SERVICE AN

758ULT 748468/

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Gaps

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Length 3457;

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Since the promoter region of the nifH operon has been isolated, characterised and cloned, it is possible to delete the nifH and nifHD nitrogenase genes and replace them with structural genes isolated from an extraneous source. The extraneous genes thus placed under the control of the nifH promoter can then be inserted into a plasmid vector followed by conjugation into a fast-growing R.
                                                                                                                                                                                                                                                                                           promoter of fast-growing Rhizobium japonicum - used to drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colon carcinoma kinase 4; CCK-4; receptor tyrosine kinase; signal transduction; colon cancer; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                            transcription in rhizobium of heterologous structural genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4216 BP; 906 A; 1254 C; 1251 G; 793 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 8; Ler
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon carcinoma kinase 4 (CCK-4) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
193..3405
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0%;
100.0%; Pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T45351 standard; cDNA; 4258 BP
                                                                                                                                                            (LUBR) LUBRIZOL GENETICS I. (LUBR-) LUBRIZOL GENETICS I.
                                                                                                                        85US-0763800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0452630.
                                                                                        86EP-0306105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3903 agctcaacctcatccac 3919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1213 agctcaacctcatccac 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag- b
271..3402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193. 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                      WPI; 1987-051801/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                  Appelbaum ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                        07-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9637610-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1996;
                                                                                                                          07-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1996
                                                   25-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
               EP211661-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T45351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 82
T45351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
ö
                                                                                                                                                                                                                                                                                                        This cDNA encodes a Xenopus protein "chordin". The functional recombinant protein chordin has a defined sequence of 941 amino acids and can induce dorsal and neural development and endodermal differentiation in vertebrates. The presence of a hydrophobic signal sequence, four possible N-glycosylation sites and conserved Cys-rich repeat regions suggest that chordin is a secreted protein. The DNA sequence can be operatively linked with an expression vector, to form a construct and a transformant can be obtained by introducing the construct into a host. Chordin may be useful as a component of culture media for culturing cells such as nerve or muscle cells, for treating neurodegenerative diseases and damaged nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                  DNA encoding Xenopus frog protein - that induces dorsal and neural development and endodermal differentiation in vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of nitrogen fixation gene H (nifH) promoter and coding region and the nifH-nifD intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3796 BP; 1046 A; 841 C; 958 G; 951 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium expression vector; plant expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Le
1.7e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 1; Pred. No. 1.7e 0; Mismatches
                                                                                                                                                                                                                                                                    Claim 1; Columns 19-22; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium japonicum strain USDA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jocation/Qualifiers
1921..1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= f
/note= "claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; So
ilarity 100.0%; P.
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N70558 standard; DNA; 4216 BP
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label= nifD
               94US-0343760
                                                   94US-0343760
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1933..1936
/*tag= b
2012..2016
/*tag= c
2024..2914
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                                                                                                                          De Robertis EM, Sasai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label=
                                                                                        (REGC ) UNIV CALIFORNIA
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                                                                                                                                                           WPI; 1997-525754/48.
P-PSDB; W31559.
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradyrhizobium; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
               22-NOV-1994;
                                                   22-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
promoter
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N70558
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WHY with Shift is a stab or of or of of the

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The present expanded cDNA sequence encodes human BAG-5 (Bcl-2 associated athanogene-5) protein. BAG is a Hsc70/Hsp70-regulating protein (Brs70/Hsp70) is a molecular chaperone that participates in controlling protein bloactivity, degradation, complex assembly/disassembly and translocation across membranes). It competes with Hip for binding to the Hsc70/Hsp70 ATPase binding domain and promotes substrate release. Gene transfection studies indicate that BAG proteins influence a wide variety of cellular phenotypes through their interactions with Hsc70/Hsp70, including increasing resistance to apoptosis, promoting cell proliferation, enhancing tumour cell migration and metestasis and altering transcriptional activity of steroid hormones. BAG also stimulates Hsc70-mediated adenosine triphosphate (ATP) hydrolysis by
proliferation, cell migration and metastasis and steroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fanconi Anemia Group C; FACC; complementing cDNA; varient; open reading frame; diagnosis; Fanconi anemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                        Sequence 4308 BP; 1201 A; 897 C; 987 G; 1222 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 17; DB 21; I
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human FACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
174..1850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANDEM
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                                                       Claim 12; Fig 17; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q51426 standard; cDNA; 4488 BP.
                                                                                                                                                                                                                                                                                                                        accelerating ADP/ATP exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0876285.
92US-0918313.
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/*tag= b
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3323..4455
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3163..3175
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3289..3322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FACC cDNA clone #1.
                 receptor function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1992;
21-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  051426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human BAG-5; Bcl-2 associated athanogene-5; apoptosis; cell migration; tumour cell metastasis; Hsc70/Hsp70-regulating protein; metastasis; tumour cell proliferation; steroid hormone receptor function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                        New isolated receptor tyrosine kinase, CCK-4 - used for developing prods. for the diagnosis and treatment of CCK-4 signal transduction disorders, partic. colon cancer
                                                                                                                                                                                                                     A cDNA sequence (745351) codes for a novel human receptor tyrosine kinase, colon carcinoma kinase-4 (W08747), or CCK-4, which is preferentially expressed in cancerous colon tissue, compared with normal colon. The cDNA sequence is a consensus of 6 overlapping cDNA clones isolated from a human placenta library using primers based on conserved motifs of protein tyrosine kinase catalytic domains. CCK-4 nucleic acids can be used in the prodn. of recombinant CCK-4 polypetides, and as probes in the diagnosis and screening of CCK-4 signal transduction disorders, esp. colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17; DB 18; Length 4258; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full length expanded cDNA sequence for human BAG-5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4258 BP; 868 A; 1252 C; 1282 G; 856 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
247.1590
/*tag- a /product- "Human BAG-5 protein"
                                                                                                                                                                                       Claim 1; Fig la-d; 129pp; English
                 Ullrich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z51806 standard; cDNA; 4308 BP
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                                                                                                                                                                                                                                                                                                                                                                                                   cancer, and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BURN-) BURNHAM INST
                 Alves F, Mossie K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-256937/22.
P-PSDB; Y70517.
                                                     WPI; 1997-021219/02.
P-PSDB; W08747.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z51806;
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51806
10 Z51806
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Gaps

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This cDNA clone includes a coding region for human Fanconi anaemia complementation group C (FAC, see W66546), a protein that modulates approcise in haematopoletic progenitor cells (HPC). The invention provides conjugates, including fusion proteins, comprising FAC and a targetting molecule which binds to a cell surface protein of the HPC and is internalised. Such targetting molecules include interleukin-3 (see W68547) and antibodies which recognise CD33 (see W68546-49). The conjugate, or a nucleic acid encoding it, can be used to deliver FAC to an HPC, specifically to inhibit apoptosis, particularly in patients exposed to high doses of chemotherapy for treatment of non-myeloid cancers, also to treat Fanconi anaemia (by complementation of the genetic defect). Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant production of conjugate in cell cultures) or in vivo. Treatment with FAC may eliminate the need for extensive bone marrow transplants to restore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 17; DB 20; Length 4567; 100.0%; Pred. No. 1.7e+02; ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4567 BP; 1080 A; 1135 C; 1177 G; 1175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Traversari C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boon T, Chomez P, De Plaen E, Lurquin C, Tra
Van Den Eynde B, Van Der Bruggen P, Van Pel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
3881..4711
/*tag= a
                        Claim 6; Page 40-45; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopolesis after chemotherapy.
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91US-0728838.
91US-0764364.
91US-0807043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q32352 standard; DNA; 5674
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nes 17; Conserv
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09-JUL-1991;
23-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in Q51426-28 represent cDNA varients from the Fanconi Anemia Group C Complementing (FACC) cDNA. These three cDNA molecules are cellular varients of a single cDNA transcribed from the same gene. The three cDNAs each contain an identical open reading frame encoding the FACC protein. The FACC protein may be used for the diagnosis and study of Fanconi anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New conjugate of Fanconi anaemia molecule and peptide selective for haematopoletic precursor cells – inhibits apoptosis of these cells, for treating Fanconi anaemia and patients undergoing high-dose chemotherapy for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementation group C; FAC; apoptosis;
bone marrow; chemotherapy; gene therapy; human; ds.
                                                                                                                                                                                                                                                                           Human cDNA which complements Fanconi Anaemia gp. C - used to develop prods. for use in diagnosis, study and therapy of Fanconi Anaemia
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                                                                                                                                                  Strathdee CA, Wevrick R;
                                                       (HOSP-) HOSPITAL FOR SICK CHILDREN.
(UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 97-101; 137pp; English.
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256..1929
/*tag= a
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100.0%; Pred
0; M
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9308-0003963.
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P-PSDB; W68546.
                                                                                                                                                                                                      WPI; 1993-368794/46.
P-PSDB; R44139.
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Best Local Similarity
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15-JAN-1993;
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                                                                                                                                                  Buchwald M,
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Matches

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mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                MAGE-1 gene
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12-DEC-1991
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X84113
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                             The sequences given in 032352-69 represent a new family of genes refered to as melanoma antigens (MAGE). The cDNAs of this gene family were identified during the isolation of the antigen E gene. The MAGE CDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA sequence. The MAGE DNAs share a certain degree of homology with each other and are expressed in tumnour cells including several types of human tumor cells as well as in human tumors. MAGE expression is not restricted to melanomas. MAGE refers to a family of tumor rejection antigen precursors. The antigens resulting from these genes are referred to as MAGE TRAS or melanoma antigen tumor rejection antigens. See also Q32351.
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q72477 is the DNA sequence which encodes melanoma antigen-1 (MAGE-1). Another melanoma antigen MAGE-3 is encoded by Q72470, this is a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytolytic T cells specific for the complex of antigen D (the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DER BRUGGEN P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3;
cancer; cytolytic T cells; antigen D; human leucocyte antigen;
                                                                                                                                                                                                                                                                                                                             Length 5674;
                                                                                                                                                                                                                                                                           Sequence 5674 BP; 1277 A; 1644 C; 1568 G; 1185 T; 0 other;
                                                                                                                                                                                                                                                                                                                           Score 17; DB 13; Length 56
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumour rejection antigen precursor MAGE3 - useful in
treatment and diagnosis of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour rejection antigen MAGE-1 encoding DNA
       Disclosure; Page 71-73; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 26; Page 59; 105pp; English.
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100.0%; Prf
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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nes 17; Conser
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Best Local &
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                                                           Length 5674;
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A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;
Seguence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other
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100.0%; Pred. No. 1.7e+02;
:Ive 0; Mismatches 0;
                                                                             1.7e+02;
                                                         Score 17; DB 15;
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P, Van Pel
                                                                                                 Mismatches
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                                                                               Pred. No.
                                            0.6%; Scor.
100.0%; Pre
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Van Den Eynde B, Van Der Bruggen
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91US-0728838.
91US-0764365.
91US-0807043.
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                                                         Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conservative
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T42117
ID T42117
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"GGGAGCGGGATCAAC insertion in genomic DNA". 3489
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/note- r in genomic sequence"
/note- r in genomic sequence"
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                                                   u
"AAC in genomic sequence"
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note= "Deleted in genomic DNA"
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"G in genomic sequence"
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"T in genomic sequence"
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|ote= "Intron-7 splice site"
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note= "Intron-4 splice site"
25..3726
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ote= "intron-5 splice site"
04..3805
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ote= "Intron-3 splice site'
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|ote= "Intron-6 splice site"
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                                                                                     Lats gene; large tumour suppressor; Drosophila melanogaster; fruitily; polydenylation site; protein serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder: trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
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note= "A in genomic sequence"
por.5720
*tag d
note= "Sequence from clone cDNA-A2"
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note= "Sequence from clone cDNA-9"
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note= "GGA in genomic sequence"
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"G in genomic sequence"
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*tag* k
note= "Intron-2 splice.site"
371..1818
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note= "Intron-1 splice site"
                                                               Lats gene encoding large tumour suppressor.
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                                    22-JAN-1997 (first entry)
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The present sequence is a DNA encoding Drosophila Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and angative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soff tissue sarcomas and ovarian tumours, and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
Fruit fly: Lats; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma: pituitary disorder; gene therapy; hyperplasia; ll; luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
                                                                                                                                                                                                                                                                                                                                                             region is identical to the 1-141
of Drosophila plc-21 transcript"
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0.6%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                     Location/Qualifiers
1103..4402
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/note= "This
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Stewart RA;
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9803-0096997
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Matches 17; Conservative
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P-PSDB; Y70393.
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Turenchalk GS,
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18-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding genomic sequence is identical, except for 34 minor differences, and has 7 introns. Two consensus polyadenylation sites are present. A 141-bp sequence at the 3'-end of the lats transcript is identical to the 5'-end of the untranslated sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated large tumour suppressor gene - used to develop prods for inhibiting cell proliferation
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/note= "AAAAGCAAATTAATAAAT in genomic sequence"
5657..5663
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/note= "GTGGCCCCCTCCCTCCTCAT in genomic
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/note= "TGTAATTAGTG in genomic sequence"
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/note= "Deleted in genomic DNA"
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"A in genomic sequence"
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5247..5253
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Matches 17; Conservative
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WO9630402-A1

03-OCT-1996

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26-MAR-1996; 27-MAR-1995;

Tao W,

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21-JUN-2000

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Query Match

Matches

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Sequences of three polymorphic human NAT genes are given in Q48767-Q48772. Detection of polymorphic human NAT genes allows diagnosis of adverse effects to be caused by amino-contg. aromatic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic human arylamine N-acetyl-transferase genes - used to diagnose adverse effects caused by amino-contg, aromatic
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computer readable medium; vaccine; pharmaceutical composition;
                                                                                              Arylamine N-acetyl-transferase; NAT; polymorphism; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6464 BP; 2087 A; 1189 C; 1282 G; 1906 T; 0 other
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Pred. No.
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                                           Arylamine N-acetyl-transferase type 3.
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723..1595
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100.0%; Pre
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V52165
ID V52165 standard; DNA; 10240 BP.
                                                                                                                     amino; aromatic substance; ds
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1800.1805
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21-APR-1994 (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
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P-PSDB; R41246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP562547-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V52165;
                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= Tumour rejection antigen MAGE-1.
/product= The CDS is not indicated in the text of the
specification but is suggested in the layout
of the sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to MAGE-1 - useful for hybridomas, recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A monoclonal antibody directed against the tumour rejection antigen (MAGE-1) can be used to detect MAGE-1 in samples by standard immunoassay methods for diagnosis and monitoring of cancer etc. The monoclonal antibody is designated MA454 and is produced by the hybridoma deposited as ATCC HBB11540. The monoclonal antibody is specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3. Peptide fragments of MAGE-1 (See R80618-20) may be useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide fragments of MAGE-1 (See R80618-20) may be useful as immunogens for production of the monoclonal antibody and antisera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boon-falleur T, Chen Y, Garin-chesa P, Old LJ; Rettig WJ; Stockert E, Van der bruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5724;
                                                                                                                                                                                                                                          antigen; MAGE-1; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5724 BP; 1282 A; 1653 C; 1589 G; 1200 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 17; DB 16; I
100.0%; Pred. No. 1.7e+02;
tve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(SLOK ) MEMORIAL SLOAN-KETTERING CANCER CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New monoclonal antibody binding specifically diagnosis and monitoring of cancer, also new MAGE-1 and immunogenic peptide(s)
                                                                                                                                                                                             Tumour rejection antigen (MAGE-1) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 16-19; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
3881..4711
                                                                                                                                                                                                                                                                    diagnosis; immunoassay; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0°;
100.0%; Pit
                                        Q98902 standard; DNA; 5724 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     048772 standard; DNA; 6464 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US00095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3994 ggtcctgggcacctgg, 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0190411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-283606/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                             Tumour rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9520974-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994;
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                            28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1995.
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Shin S;

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Gaps

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Indels

Streptococcus pneumoniae.

Query Match Best Local S Matches 17

048772

SESULT 92

. 18772

DB 14; Length 6464; 1.7e+02; hes 0; Indels

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Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                  New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X20500-21243 represent polynucleotide sequences from the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10461 BP; 2325 A; 3411 C; 2493 G; 2213 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 17; DB 20; 1
.00.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 491-497; 1150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V74675 standard; DNA; 10813 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                             98WO-US13041.
                                                                                                                           97US-0050667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6768 gcggcacctgcgcacgc 6784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 geggeacetgegeacge 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999 .(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxic shock syndrome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
                                                                                                                                                                                                                                                                                     WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                           23-JUN-1998;
                                                                                                                         24-JUN-1997;
                          30-DEC-1998
                                                                                                                                                                                                                                    Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
V74675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded to nit, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S: pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologue to amplification primers derived from the sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the supermoniae genome of commercial importance, or expression modulating fragments of the supermoniate genome. Products from the present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                        Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 19; Length 10240;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10240 BP; 2865 A; 1914 C; 2390 G; 3068 T; 3 other;
                                                                                                                                                                                                                                                            Fannon M;
                                                                                                                                                                                                                                                            Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 326-332; 1409pp; English.
                                                                                                                                                                                                                                                            Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.00.
100.08; Fix
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                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                      97WO-US19588.
                                                                                                                                                         960S-0029960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7643 gatttggaagagtttca 7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                          Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                        WPI; 1998-272225/24
WO9818931-A2
                                                                                                      30-0CT-1997;
                                                                                                                                                         31-OCT-1996;
                                                   07-MAY-1998
                                                                                                                                                                                                                                                            Barash SC,
Kunsch CA,
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pneumoniae

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Gaps

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0; Indels

Length 10461;

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these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering
                                                                                                                                                                                                                                        /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence 2101..2160
                                                                                                                                                                                                                                                                                                                           /*tag= b // note= These bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence
                                                                                       Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                          Staphylococcus aureus contig SEQ ID #364.
                                                                                                                                                                                                   Location/Qualifiers
301..360
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                      "these bases
                                                                                                                                                                                                                                                                                                                                                                                                          3901..3960
                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature 🟗
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Treponema pallidum infection; syphilis; Borrelia infection; animal; ... enzyme production; ds.

Treponema pallidum WO9859034-A2

具者具备用者医内容等

X20553;

TESULT 94 120553

(first entry)

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Rat nestin gene - its product is useful to identify brain tumours
                                                           Q70447 standard; DNA; 11236 BP
                                                                                                                                                                                          21-MAR-1995
                                                                                                                           070447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osciencempelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence?
                                                                                                                                                                                                                                                                                                                  "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
given in the specification for this DNA sequence. 5701...5760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus
in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; Length 10813; 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10813.BP; 3513 A; 1895 C; 1594 G; 3451 T; 360 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 1; Pred. No. 1.7e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1248-1254; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC, Choi GH, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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/*tag= f
/note= "thes
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/note= "t]
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Best Local Similarity 100
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-374922/35.
                                                               misc_feature
                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Q70447 is the rat nestin gene encoding nestin protein (R60126).
Nestin protein expression distinguishes neural multipotential stem
cells and brain tumour cells from the more differentiated neural.
cell types (eg., neuronal, glial and muscle cells of the adult brian).
                                                           nestin gene; brain tumour; neoplastic cells; glial; neuronal; muscle; neural multipotential stem cell; mammalian brain; detection; diagnosis; medulloblastoma; gliablastoma; oligodendroglioma; ds.
                                                                                                                                                                                                                      'transl_except= pos:3087..3091, aa:His, Arg
'note= "sequence should be CAY CGG, ie. Y or C has
been deleted in the sequence given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brain tumour
in the
                                                                                                                                                                                                                                                                /*tag= d
/note= "apparent inclusion of a nucleotide"
3375..4339
                                                                                                                                    /*tag= a
/note= "start of primary transcript"
2589..10821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide and protein sequences for human and rat distinguishes neural multipotential stem cells and cells from more differentiated cell types; for use
                                                                                                                                                                                         Nestin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 25-34; 45pp; English.
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0180548.
88US-0201762.
90US-0603803.
91US-0660412.
                                                                                                                                                                                                                                                                                                                                                                    6194..6388
/*tag= 1
6389..10821
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6120..6193
/*tag= h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis of brain tumours
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4465..6
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                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lendahl U, Mckay RDG;
                                                                                                                                                                                                                                                      3104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-263332/32.
P-PSDB; R60126.
                                                                                                      Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1988;
25-OCT-1990;
22-FEB-1991;
                                                                                                                           Key
misc_feature
                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                          US5338839-A.
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Gaps

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Indels

Werner's syndrome; detection; diagnosis; autosomal; isorder; phenotype; ss.

recessive disorder; phenotype;

Mouse; WRN;

WO9724435-A1 Mus musculus

Partial mouse WRN genomic sequence #1.

(first entry)

31-AUG-1999

x83005;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for Tr pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
The nestin protein can be used in diagnosing tumours of the brain, such as medulloblastomas, gliablastomas and oligodendroglioma. (See also Q70448).
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 17; DB 20; Length 21170;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels 0
                                                                                                                        Length 11236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21170 BP; 4629 A; 5015 C; 6107 G; 5390 T; 29 other;
                                                                       Sequence 11236 BP; 2876 A; 2678 C; 3258 G; 2424 T; 0 other;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production of biosynthetic products such as enzymes
                                                                                                                        Score 17; DB 15;
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 389-401; 1150pp; English.
                                                                                                                                                                                                                                                                                                     15/c
X20535 standard; DNA; 21170 BP.
                                                                                                                        Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US13041.
                                                                                                                                                                                           2 3466 ccttcaggaagggctg 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0050667
                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9859034-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser CM;
                                                                                                                                                                                                                                                                                                                                                      x20535;
                                                                                                                                                                                                                                                                                 SSULT 97
                                                                                                                                                                                                                                                                                                     .20535,
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                                                                                                                                                                                                                                                                                                                                                                                                          我的知意是因的是是最近的特殊的特殊的人,就是自己的特殊的自己的自己的人员
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Isolated nucleic acid molecule encoding the WRN gene product . useful for detection and treatment of Werner's syndrome, and related

ΰ Υū

Schellenberg GD,

Oshima J,

Fu Y,

WPI; 1997-363671/33 Mulligan J,

MOLECULAR CORP

DARW-) DARWIN (OSHI/) OSHIMA

96US-0594242

96US-0632175. 95US-0009409. 95US-0580539. 96US-0010835.

29-DEC-1995; 30-JAN-1996;

30-JAN-1996;

96WO-US20785

30-DEC-1996;

12-APR-1996 39-DEC-1995

10-JUL-1997

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This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (X83004). The corresponding human gene (X83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAV-3; defective recombinant PAV vector; live recombinant virus; subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; oytic fibrosis; cancer; viral infection; acquired immune deficiency syndrome; PAV antigen; porcine pathogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 18; Length 29604;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29604 BP; 7634 A; 5861 C; 5985 G; 10123 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete nucleotide sequence of the PAV-3 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 7; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53/c
Z30163 standard; DNA; 34094 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine adenovirus Type 3. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as well as related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525 aaaggaatagaactggc 541
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Best Local Similarity 100.
Matches 17; Conservative
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Gaps

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:ESULT 98 :23005) X83005 standard; DNA; 29604 BP.

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17; Conservative

Best Local Similarity Matches 17; Conservat

Query Match

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(UYSA-) UNIV SASKATCHEWAN,
                      WPI; 1999-620422/53
       15-APR-1999;
           15-APR-1998;
   21-0CT-1999
                   Reddy PS,
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Babiuk LA;

Tikoo SK,

99WO-US08220 98US-0081882

WO9953047-A2

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The present sequence represents the complete nucleotide sequence of the genome of porcine adenovirus-3 (PAV-3). The specification also describes a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate inefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3 increases the size of heterologous insert that can be packaged. The PAV-3 increases to polynucleotides sequences are used to produce (recombinant or defective) vectors that can express heterologous proteins, e.g. for making live, recombinant virus or subunit vaccines, for nucleic acid immunisation or for gene therapy (e.g. of genetic diseases such as hemophilia or cystic fibrosis, cancer, or viral infections, including acquired immune deficiency syndrome), also for in vitro expression of recombinant antigens (for antibody production), antisense RNA, ribozymes or therapeutic proteins. They are also used diagnostically to detect PAV antigens and/or nucleic acid. The vectors may be used in human or veterinary medicine, but particularly for expressing protective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 veterinary medicine, but particularly for expressing protective determinants of porche pathogens. Regulatory regions may be used to control expression of heterologous genes. Antibodies raised against PAV-3 polypeptides can also be used for diagnosis (to detect PAV-specific
New nucleic acids from the genome of porcine adenovirus-3, and derived gene therapy vectors, particularly for immunization
                                                                                                                                                                                                        Example 2; Fig 1; 87pp; English
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Gaps ö Length 34094; 0; Indels 0.6%; Score 17; DB 20; 1 100.0%; Pred. No. 1.6e+02; Mismatches .; 0 330 ctcatgcaggagcacaa 346 Conservative Query Match Best Local Similarity >

Sequence 34094 BP; 6240 A; 11070 C; 10693 G; 6091 T; 0 other;

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Gaps

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Indels

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Conservative

Similarity

Query Match Best Local Simi: Matches 17;

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Search completed: February 18, 2001, 16:04:40 Job time: 25989 sec

Db 37241 GGTGACCGGCGGCTTTC 37225

11 ggtgaccggcggctttc 27

δλ

Length 38734;

Score 17; DB 20; 1 Pred. No. 1.6e+02;

0.68;

Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;

4686 CTCATGCAGGAGCACAA 4670 d.

0/c Z32020 standard; DNA; 38734 BP. SESULT 100

(first entry) 10-JAN-2000 232020;

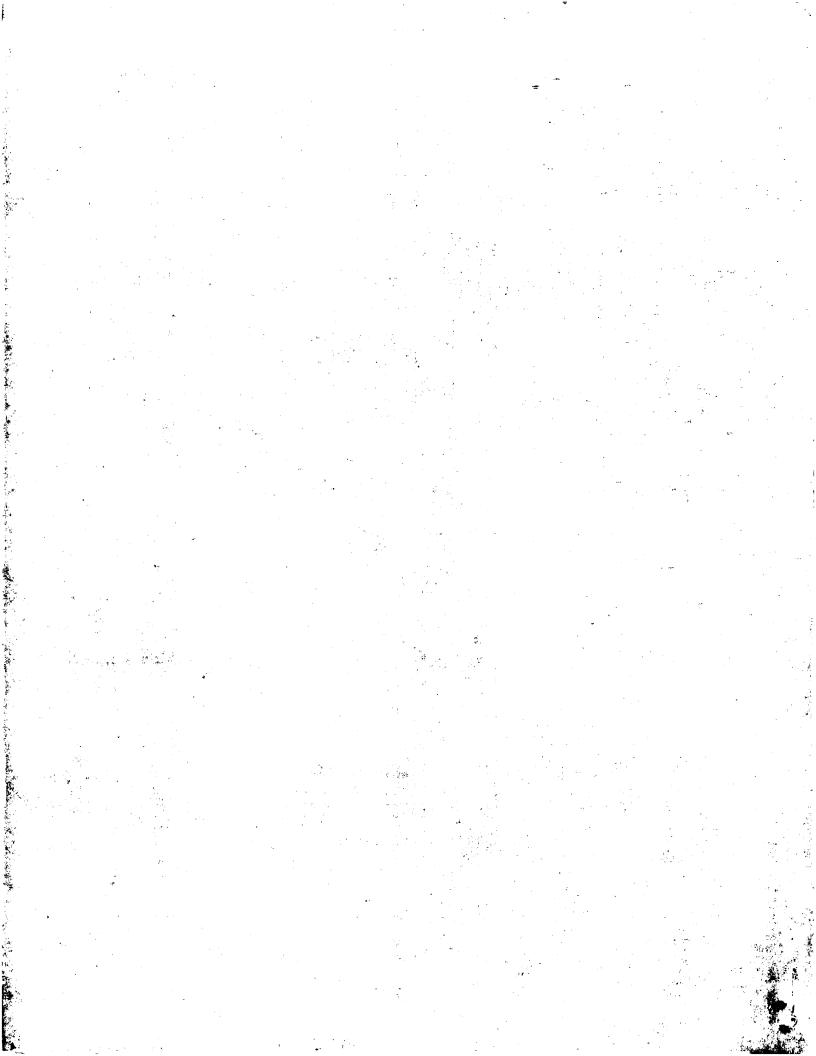
Human METH1 related EST AL021529.

Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; hemmatolid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.

sapiens Ношо

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They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders, acquired (e.g. by chemothars) cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. 232002 to 232080, and 149503 to represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                       New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemanglomas, and arterlal-venous malformations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             232000 and 232001 encode, and Y49501 and Y49502 represent, human
                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 296-321; 457pp; English.
                                                                                                                                                                                                                                                            Iruela-Arispe L, Hastings GA,
                                                                              99WO-US01313.
                                                                                                                    98US-0072298.
98US-0098539.
                                                                                                                                                                                (IRUE/) IRUELA-ARISPE L.
                                                                                                                                                                                                    HASTINGS G A.
                                                                                                                                                                                                                                                                                                WPI; 1999-590684/50.
                                                                                                                                                                                                                     (RUBE/) RUBEN S M.
W09937660-A1
                                                                            22-JAN-1999;
                                                                                                                  23-JAN-1998;
28-AUG-1998;
                                       29-JUL-1999
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US-08-639-075A-104
PCT-US95-14442A-104
US-08-611-757-98
PCT-US95-05980-98
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US-07-789-738-3
US-07-789-738-3
US-08-651-136C-15.
US-08-906-769-128
US-08-906-616-128
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US-08-687-080-70
US-08-630-822A-97
US-09-005-069-97
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US-08-651-136C-17
US-08-933-750C-81
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                                      US-08-190-411A-1
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US-08-507-016-8
PCT-US91-06418-4
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/cgnl_7/ptodata/1/ina/c_COMB.seq:*
/cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
/cgnl_7/ptodata/1/ina/packfiles1.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-878-546-9
US-08-877-101-23
US-08-957-101-23
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US-08-101-101
US-08-101-109
US-08-101-109
US-08-993-118-8
US-08-993-118-8
US-08-951-148-2
US-08-951-148-2
US-09-574-576-2
US-08-951-148-2
US-08-951-148-2
US-08-951-148-2
US-09-101-234-2
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                                                                                                                                                                                                                                                  February 18, 2001, 07:28:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sost-processing: Listing first 100 summaries
                                                                                                                                                           nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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2958
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Match
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No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 19; Conservative
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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            IRY: Canada
M5G 1R7
Ontario
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US-08-867-941-6
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APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Lactorerrin receptor genes of Moraxella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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Patent No. 5977337
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: Du, Kun-Pan
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michal H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 2955; 7.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/867,941
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
6th Floor, 330 University Avenue
                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19;
                                                                                                             Sequence 9, Application US/08867941 Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    Loosmore, Sheena
Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 TCTTGGTGCTCAAAGCAAA 609
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2955 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811 tettggtgeteaaageaaa 829
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Best Local Similarity 100.
Matches 19; Conservative
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EDNESS: single
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CITY: Toronto
STATE: Ontario
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M5G 1R7
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-S-08-867-941-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESULT 2
-5-08-867-941-8
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5: Sim & McBurney 6th Floor, 330 University Avenue

CORRESPONDENCE ADDRESS

ADDRESSEE:

STREET: burre

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Gaps
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APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3000;
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN 1997
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MİS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1156
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FLING DATE: US/08/867,941
FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Sim & MoBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUWTRY: Canada
ZIP: M5G 1R7
COMPUPP TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 2;
Pred. No. 7.5;
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,'
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
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Sequence 3, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                        STATE: Indiana COUNTRY: United States of America ZIP: 46285
                                                                                                                                                                            STREET: Lill Corporate Center
CITY: Indianapolis
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Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Cates, Melvyn
APPLICANT: Lill Lilly and Company
STREET: Lill Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
ZIF: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE:
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bred. No. 23;
Mismatches 0;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-113'
TELECOMMUNICATION INFORMATION:
TELEFRONE: (317) 276-0756
TELEFRONE: (317) 276-0756
TELEFRAX: (317) 276-3861
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 base pairs
TYPE: nucleic acid
                                                                                                                                                0.6%; Scor
100.0%; Pre
0;
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                                                                                                                                                                                                                                      811 tcttggtgctcaaagcaaa 829
        SEQUENCE CHARACTERISTICS:
LENGTH: 7641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                          Query Match 0.69
Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.'
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Indianapolis
STATE: Indiana
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LOCATION:
US-09-045-186-1
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38-09-045-186-1/c
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Length 1152;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/045,186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIBANO, YUJI
APPLICANT: KIKUCHI, NORIHISA
APPLICANT: ODA, KOHEI
TITLE OF INVENTION: NOVEL PROTEINASE INHIBITOR ATITLE OF INVENTION: GENE ENCODING THE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RASKIN & DAVIDSON P.C.
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red. No. 23;
Mismatches
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100.0%; Pr
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US-08-878-546-9
; Sequence 9, Application US/08878546
; Patent No. 5952463
                                                                                                                                FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGIETAATION NUMBER: 36,808
REFERENCE/DOCKET UNMBER: P-11
TELECOMMUNICATION INFORMATION:
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IBM PC compatible
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEINBERG
                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: mRNA
US-09-045-186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                     TELEPHONE:
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RESULT 5 TS-09-045-186-3/c

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APPLICATION NUMBER: US/08/967,101
FILING DATE: IO-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ore 18; DB 2;
red. No. 23;
Mismatches 0
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APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, DAUL E
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PRO'
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSE:
ADDRESSET: High Street Tower' - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
FLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Revin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-967-101-23/c
; Sequence 23, Application US/08967101
; Patent No. 5840540
                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; So
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1421 TTCCAAAGTGTGTACTTT 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
COTHER INFORMATION:
US-08-680-395-4
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: - LOCATION: 1..2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gray, Joe W.
APPLICANT: Glins, Colin
APPLICANT: Godfrey, Tony
APPLICANT: Rowbel, David
APPLICANT: Rowbel, David
APPLICANT: Rowbel, David
APPLICANT: Rowbens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 18; DB 2; Length 2186;
100.0%; Pred. No. 23;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 23;
Mismatches
                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 158677/1996
FILING DATE: 19-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 24104/1996
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 48101/1997
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVIDSON, CLIFFORD M.
REGISSPRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 32,728
REFERENCE/COCKET NUMBER: 32,728
REFERENCE/COCKET NUMBER: 32,728
REFERENCE/CREATION:
TELECHHONE: (212)-768-3800
INFORMATION: TELEPHONE: (212)-768-3800
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  APPLICATION NUMBER: US/08/878,546 FILING DATE: 19-JUN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: STREPTOMYCES PLATENSIS
STRAIN: Q268
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Sequence 4, Application US/08680395
Patent No. 5892010
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1652 ggtcctgggcaccctggc 1669
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Best Local Similarity 100.0
...thes 18; Conservative
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
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LOCATION: 1477..1911
.3-08-878-546-9
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CITY: San Francisco
STATE: California
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ANTI-SENSE: NO
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APPLICANT: Kim, Jungsuh P.
APPLICANT: Reyes, Gregory R.
APPLICANT: Wades, John
APPLICANT: Vang-Keck, Zhen-Yang
APPLICANT: Young, LaVonne
TILLE OF INVENTION: No. 5859230-A/No. 5859230-C/No. 5859230-D/No.
GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
183
                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                 HURWITZ & THIBEAULT
et Tower - 125 High Street
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350 Cambridge Avenue, Suite 250
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100.0%; Pred. No.
:ive 0; Mismatc
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 20, Application US/08611757; Patent No. 2859230 (GENERAL INFORMATION: APPLICANT: Kim, Jungsuh P.
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
US-09-124-698-23
                                                                                                                 High Street Tower
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LENGTH: 289 base pairs
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                                                                                                                                                    Massachusetts
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CORRESPONDENCE ADDRESS:
                                                            NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HUI
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 17; Conserva
                             FITLE OF INVENTION:
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                                                                                                                                     Boston
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US-08-611-757-20/c
                                                                                                                                                                                                                                                                                                                                  FILING DATE
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              APPLICANT:
                                                                                                                 STREET:
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Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAULE
TITLE OF INVENTION: GENERIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURMITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
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                                                                                                                   Length 289;
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                                                                                                                                                    Indels
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                                                                                                                 DB 2;
71;
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71;
                                                                                                    0.6%; Scor.
100.0%; Pred. No. ...
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PICCHE, EGMUNG R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic): 5-08-967-101-23
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                                                                                                               Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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nucleic acid
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STATE: Massachusetts
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              single
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              STRANDEDNESS:
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Length 289; Indels

DB 3; 71;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 72,
                                                                                                                                                                                                                     ANTI-SENSE: NO
CONGINEL SOURCE:
INDIVIDUAL ISOLATE: NY 190 Clone D30
PCT-US95-05980-20
                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17;
100.0%; Pred. No.
:ive 0; Mismatc
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100.0%; Pre
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINAL
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,600
REFERENCE/DOCKET NUMBER: 45.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 110:
TELECOMMUNICATION INFORMATION
        ILLEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INPORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
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                                                                                                                                                                                                                                                                                                                                                                                                                       132 egcegegageggeegeg 148
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                     nucleic acid
                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-A/Non-B/Non-C/Non-D/Non-E Hepatitis
Agents and Molecular Cloning Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05980
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE: INDIVIDUAL ISOLATE: My 190 Clone D30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17;
Pred. No.
                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: 05.396
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/922,493
FILING DATE: 30-UL1-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 4600-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,986
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0203
REFERENCE/DOCKET NUMBER: 4600-0203
APPLICATION NUMBER: US/08/611,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TESULT 12
TT-US95-05980-20/C
Sequence 20, Application PC/TUS9505980
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 cgccgcgagcggccgcg 148
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 304 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 cecceceaeceecece 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO TITLE OF INVENTION: AG NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 350 Camt
CITY: Palo Alto
STATE: CA
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MOLECULE TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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APPLICANT:
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Length 1094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/458,356
FILLOATION DATE: 02-JUN-1995
                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer: #111am S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
3: Curtis, Morris & Safford
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       имвек: US/08/184,009
19-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 109, Application US/08458356
Patent No. 5942235
                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
ITLE OF INVENTION: RECOMBINAL
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 42506GURTMS
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1652 ggtcctgggcaccctgg 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 base pairs
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-JAN-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM_TYPE: Floppy
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                     New York
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10036
Pr
                                                                              USA
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  ADDRESSEE:
                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
Apprication: 424
Apprication: 424
Apprication: 424
Apprication: 424
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Patent No. 5833975
GENERAL INFORMATION
APPLICANT: Paclett, Enzo
APPLICANT: Tartaglia, James
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
                                                                                                                                                                                                                 APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECHONE: (212) 840-3333
TELEPAN: (212) 840-0712
TELEFAX: (212) 840-0712
TELEX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                       E: Curtis, Morris & Safford
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                    Sequence 110, Application US/08458356
Patent No. 5942235
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOSAME-PRING TRANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1652 ggtcctgggcacctgg 1668
                  1652 ggtcctgggcacctgg 1668
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                                                          292 GGTCCTGGGCACCCTGG 308
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        10036
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                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-458-356-110
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Gaps

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Indels

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Mismatches
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                                                                                                                                                                                                        Sequence 8, Application US/08845528C Patent No. 6027924
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMEY, Charles;
APPLICANT: BOON-FALLEUR, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/08951148
; Patent No. 5871973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; So
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
  Best Local Similarity 100.0%; F
Matches 17; Conservative 0;
                                                              1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1652 ggtcctgggcaccctgg 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York City
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New Y STATE: New COUNTRY: US ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 80
                                                                                                                                                                                       US-08-845-528C-8
                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET, Charles;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                     Length 1094;
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette, 3.5 inch, 360 kb storage IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528
FILING DATE: April 25, 1997
ATTORNEY AGENT INFORMATION:
, NAME: MATY ANNE Schoffeld
REGISTRATION NUMBER: 36,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Worderfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
REGISTRATION NUMBER: 25,506
REFREENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEFAX: 425066CURTANS
INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08993118 Patent No. 5997872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 805 Third Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                       1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 GGTCCTGGGCACCCTGG 330
                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0
Matches 17: Conservative
                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotides
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                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                TOPOLOGY: 1i
MOLECULE TYPE:
:S-08-458-356-109
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Length 1691;

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TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES TITLE OF INVENTION: THEREOF COMMENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
OPPERTING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLE OF INVENTION: CELL DIVISION REGULATORS NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lal, Pre
APPLICANT: Shah, Pu
TITLE OF INVENTION:
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Length 1816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/274,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,148
                                               APPLICATE
FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09274570 Patent No. 6121019
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ATTORNET/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 GGAAACTICTIGGIGCT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
                                                                                                                                                                                            TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                               SPLNFZT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: lines
IMMEDIATE SOURCE:
LIBRARY: SPLNFZ
CLONE: 26459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94304
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-165-234-2
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US-09-274-570-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SUFTWARE: FastSEO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,234
                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,148
FILING DATE: Herewith
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         Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09165234 Patent No. 5928899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.6%; So
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
ADDRESSEE: Incyle ... 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717 GGAAACTTCTTGGTGCT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        804 ggaaacttcttggtgct 820
                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLNFZT01
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                       STREET: SIGNITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto, STATE: CA
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TOPOLOGY: LILL
IMMEDIATE SOURCE:
LIBRARY: SPLNF?
TONE: 26459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                COUNTRY:
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FILING DATE

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Gaps

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GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 17; DB 1; Length 2419;
100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATE: 1-SEPTEMBER CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/037,230
APPLICATION NUMBER: 08/037,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanson, No. 5612201man D.
                                                                                                                                  Sequence 7, Application US/08299849B Patent No. 5612201
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                         805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: genomic DNA US-08-299-849B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1652 ggtcctgggcacctgg 1668
                                     739 GGTCCTGGGCACCCTGG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                             New York City
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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Best Local Similarity
Matches 17, Conserv
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                                                                                                                                                                                               Length 1816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors,
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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                                                                                                                                                                                                                                          Mismatches
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CURRENT APPLICATION DATA:
APLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
MINNEY: USEGN OF ANY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INCORMATION:
TELEFONE: (212) 838-384
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 5342774man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/07807043B Patent No. 5342774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                   717 GGAAACTICTIGGIGCI 733
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.*
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                 LIBRARY: SPLNFZT01
CLONE: 26459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                    CLONE: 2
LENGIH:
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APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
CORRESPONDENCE: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/804,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAISON, NO. 6025474man D.
REFERENCE/DOCKET NUMBER: LUD 5353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/967,727
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100.08;
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APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                       ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: genomic DNA US-08-967-727-7
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                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
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DNESS: single
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Best Local Similarity
Matches 17; Conserve
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                          IBM
                                                                                                                                                                                                          STATE: New TATE: New TATE: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-465-167A-23-
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                                                                                                                              GENERAL INCORNATION:

GENERAL INCORNATION:

APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Under Since, Beno t; Van Pel, Aline; De Plaen, Etienne;

APPLICANT: Lurguin, Christophe; Chomez, Patrick; Traversari, Catia

TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

TITLE OF INVENTION: Rejection Antigens and Uses Thereof

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 5925729man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 52
TELECOMMUNICATION INPORMATION:
                                                                                       Sequence 7, Application US/08142368A
Patent No. 5925729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08967727
Patent No. 6025474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1652 ggtcctgggcaccctgg 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2419 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739 GGTCCTGGGCACCCTGG 755
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .s-08-142-368A-7
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US-08-967-727-7
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Gaps
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N. tabacum cv. Xanthi
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100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application US/08343760A; Patent No. 5679783; GENERAL INFORMATION: TOSPICANT: Description Applicant: Description Title OF INVENTION: Tissue Differentiation Affecting TITLE OF INVENTION: Factor and Composition NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: Majestic, Parsons, Siebert & Hsue STREET: Four Embarcadero Center, Suite 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,760A
FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from 1 to 143 bp: Leader
non translated 5 sequence (leader)
from 144 to 2855 bp: coding sequence
for nitrate reductase apoenzyme
from 2856 to 3457 bp: non translated
3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/FR 93/00222
FILING DATE: March 5, 1993
APPLICATION NUMBER: 92 02658
FILING DATE: March 5, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20,958
REFERENCE/DOCKET NUMBER: 27209/DBP
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      LENGTH: 3457 base pairs
TYPE: nucleotide with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
CELL LINE:
                   US/08/295,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                 (1.vi.A)
(1.vi.B)
XHFD 8
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Best Local Similarity 100.
Matches 17; Conservative
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
              APPLICATION NUMBER: FILING DATE:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: S
TOPOLOGY: Linea
MOLECULE TYPE: CD
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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LOCATION:
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STATE: C.
COUNTRY:
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Pred. No. 73;
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PLANT PRECOCITY AND/OR REDUCING THE
STORED NITRATE CONTENT OF A PLANT
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended) NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/103,623
ATTORNEY/AGENT INFORMATION:
NAME: PATENTIAN NUMBER: 31,990
REGISFRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 11,990
                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 73;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Christie, Parker & Hale
STREET: P.O. Box 7068
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08295882 Patent No. 5569833 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: PLAN
TITLE OF INVENTION: STOR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                             ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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ZIP: 91109-7068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 626..1552
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SOFTWARE: WORD PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
US-08-465-167A-23
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Gaps
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                                                                                                                                                                                                                                                                                                                       Length 4488;
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APPLICANT: BOOD, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigens and Uses Thereof
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                           CHOMOSOME/SECMENT: (of corresponding genomic gene)
CHOMOSOME/SECMENT: 9q
MAP POSITION: 22.3
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
ZIP: 1002
ZIP: 1002
MEDIUM TYPER FRADABLE FORM:
MEDIUM TYPER: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                       ore 17; DB 1;
Pred. No. 73;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 3-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: HARDSON, NO. 53427/4man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REDENOMONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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    CDNA to mRNA
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805 Third Avenue
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5674 base pairs
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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STRANDEDNESS: Singular
                                                                                          ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: Human cDNA
POSITION IN GENOME: (of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: MAGE-1 gene
US-07-807-043B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 rull
CITY: New York City
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                                                                       ORIGINAL SOURCE:
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                                               ANTI-SENSE:
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ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh & ADDRESSEE: Whinston, LLP
STREET: 121 S.W. Salmon, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Buchwald, Manuel
APPLICANT: Strathdee, Craig A.
APPLICANT: Strathdee, Craig A.
APPLICANT: Wevilck, Rachel
APPLICANT: Mathew, Christopher George Porter
TITLE OF INVENTION: Fanconi Anemia Type C Gene
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TREE DISK, 3+-inch
MEDIUM TREE DISK, 3+-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORDER: US/08/441,430
FULICATION NUMBER: US/08/441,430
FILING DATE: M915, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/876,285
FILING DATE: APPLICATION NUMBER: U.S. 07/818,313
FILING DATE: July 21, 1992
APPLICATION NUMBER: U.S. 08/003,963
FILING DATE: July 21, 1992
APPLICATION NUMBER: U.S. 08/003,963
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD OF POLICY, DEFENDENCE TO NUMBER: S8,107, 1093
REGISTRATION NUMBER: 28,107
PRESIDENCE TO NUMBER: 28,107
PRESIDENCE TO NUMBER: 28,107
PRESIDENCE TO NUMBER: 28,107
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100.0%; Pred. No. ...
0; Mismatches
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REGISTRATION NUMBER: 28,758
REPERRINCE/DOCKET NUMBER: 3100.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 362-556
TELEPAX: (415) 362-5418
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08441430 Patent No. 5681942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPANE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036 CTCTACGTCTTCTCCGA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                       270 ctctacgtcttctccga 286
                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%
Best Local Similarity 100.1
Matches 17; Conservative
                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA:S-08-343-760A-1
                                                                                                                                                                                                                                    linear
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COUNTRY: U.S.A
ZIP: 97204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
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                                                                                        0.6%; Score 17; DB 1; Length 5674;
100.0%; Pred. No. 73;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM
COMPUTER: IEM
SOFTWARE: WORDER-FECT
SOFTWARE: WORDER-FECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 48
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/807,043
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-SAP-1991
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTONNEY/AGENT INFORMATION:
TELEFONDEN (212) 688-9200
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
...E.: Felfe & Lynch
...ET: 805 Third Avenue
TY: New York City
TE: New York
.10022
                                                                                                                                                                                                                                                                     3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                             1652 ggtcctgggcaccctgg 1668
                                                                                        Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: MAGE-1 gene
US-08-299-849B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 80
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
US-08-299-849B-8
US-08-190-411A-1
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                                                                                                                                                                                                                                                                                                                                                                               "Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

RAPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Old, Lloyd Selection Plerre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J

TITLE OF INVENTION: WONOCLONAL ANTIBODIES WHICE BIND TO

TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
STREE: 805 Third Avenue

CITY: New York City
                                                                                                                             Gaps
                                                                                                                             ó
                                     ore 17; DB 1; Length 5674;
red. No. 73;
Mismatches 0; Indale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New rork
STATE: New York
ZIP: 10022
COMPUTER ROADALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
"TOTAL TYPE: DISKETTE, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: US-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION 136
PRIOR APPLICATION OF 137,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/087,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 23-MAY-1991
APPLICATION NUMBER: 21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5541104man D. REGISTRATION UNBER: 30,946
REFERRINGE/DOCKET NUMBER: LUD 53
TELECOMMUNICATION INFORMATION:
                                                                100.001
100.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 5674 base pairs
nucleic acid
EDNESS: single
                                                         Query Match 0.69
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MAGE-1 gene
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Gaps
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APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Boon-Falleur, Thierry; Van der Brugen, De Plaen, El
APPLICANT: Unrquin, Christophe; Chomez, Patrick; Traversari, C
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDERS: 26
CORRE
                                                                                                                                                Length 5674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                            DB 2;
73;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 5925729man D. REGISTRATION UNBERS: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
ATTORNEY/AGENT INFORMATION:
NOME: HAUGH DATA: 129-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAUGH DATA: 07/05,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAUGH DATA: 07/05,702
FILING DATE: 23-MAY-1991
NAME: HAUGH DATE: 23-MAY-1991
NAME: HAUGH DATE: 23-MAY-1991
                                                                                                                                                    Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08142368A Patent No. 5925729
                                                                                                             0.6%; Scur.
100.0%; Pre
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                                                                                                                           3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5674 base pairs
                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MAGE-1 gene
MAGE-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York City
STATE: New York
ZIP: 10022
, NAME/KEY:
US-08-560-024-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-142-368A-8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J.
ITILE OF INVENTION: WONOCLONAL ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
ITILE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
                                                                                                                 Gaps
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                                   DB 1; Length 5674; 73;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITA:
CITA:
STATE: New YOLK
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S/08/190,411
FILING DATE: 01-FEBRUARY-1994
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JOLY-1991
APPLICATION NUMBER: 3-MAY-1991
ATTORNEY/AGENT NUMBER: 3-MAY-1991
                               ch 0.6%; Score 17; 1 Similarity 100.0%; Pred. No. 17; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE DOCKET NUMBER: LUD 5354
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucled acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,024
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 5843448man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08560024 Patent No. 5843448 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: genomic DNA
                                                                                                                                                                                       1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                          3994 GGTCCTGGGCACCCTGG 4010
                                                                          Best Local Similarity
Matches 17; Conserv
                                       Query Match
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Gaps
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                                                                                                                                                                                                                                                   APPLICANT: DEGUCHI, Takeo
APPLICANT: KINOSHITA, Moritoshi
APPLICANT: RATSURAGI, Kiyonori
APPLICANT: HIN, Sadahito
TITLE OF INVENTION: HUMAN ARYLAMINE N-ACETYLTRANSFERASE
TITLE OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,478
FILING DATE: 11-0CT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sughrue, Mion, Zinn, Macpeak & Seas 2100 Pennsylvania Avenue, N.W.
ö
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,667
FILING DATE: 23-MAR-1993
APPLICATION NUMBER: UP 64669/1992
FILING DATE: 23-MAR-1992
TELECOMGUNICATION INFORMATION:
TELECHORE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States
ZIP: 20037-3202
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               MESUL: 1-478-6; Sequence 6, Application US/08321478; Sequence 6, Application US/08321478; Pafent No. 5527677
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Querý Match 0.6%; Sc
Besť Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                           1652 ggtcctgggcaccctgg 1668
                                                                                    3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1032 aggtaccaaggaaaggc 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 293-706
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
1794..1799
17; Conservative
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1800..1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
723..1595
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SughrusTREET: 2100 Penr CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-321-478-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
Matches
                                                                                                                                                                                                                                                                                                     APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                 ö
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5674;
               Length 5674;
                                                               0; Indels
                    DB 2;
73;
                  Score 17; DB 2
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 17;
Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 6025474man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFFILIANT NUMBER: 0/780/,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/74,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                            Sequence 8, Application US/08967727
Patent No. 6025474
                  Ouery Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                          3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: genomic DNA
                                                                                                          1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MAGE-1 gene
3-08-967-727-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                     TESULT 35
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Mulligan, John T.

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0.6%; Score 17; DB 3; Length 29604; NO.0%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 68750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                    Schellenberg, Gerald D.
FENTION: GENE AND GENE PRODUCTS RELATED TO
FENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 34.317
REFERENCE/POCKET NUMBER: 240052.419
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 17; DB 3; Best Local Similarity 100.0%; Pred. No. 75; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                            STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTEMARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 39
US-09-335-409-1/c
; Sequence 1, Application US/09335409
; Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Sorangium cellulosum
US-09-335-409-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 29604 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 aaaggaatagaactggc'541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
APPLICANT: Mulligan, APPLICANT: Schellenber TITLE OF INVENTION: GTTTLE OF INVENTION: WUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                      ADDAL.
STREET: 6300
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-781-891-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 68750
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                                                                                                                                                  APPLICANT: McKay, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression As An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BELLCATION NUMBER: US/07/853,913
FILING DATE: 19920319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/603,803
PRIOR APPLICATION NUMBER: US 07/603,803
PRIOR APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-JUN-1988
PRIOR APPLICATION NUMBER: US 07/201,762
ATORNEY/AGATION DATA:
APPLICATION NUMBER: US 07/180,548
ATORNEY/AGATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Sequence 207, Application US/08781891
Setent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
                                                                                   Sequence 1, Application US/07853913
Patent No. 5338839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .y 1877 ccttcaggaagggctg 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3466 CCTTCAGGAAGGGGCTG 3482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11236 base pal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: doub.
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Gaps

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GENERAL INFORMATION:
APPLICANT: Miyata, Shohei
APPLICANT: Myata, Shohei
APPLICANT: Obshima, Atsushi
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: MATHOD FOR SYNTHESIZING STABLE
TITLE OF INVENTION: SINGLE-STRANDED CDNA IN EUKARYOTES BY MEANS OF A BACTERIAL
TITLE OF INVENTION: RETRON, PRODUCTS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 16; DB 1; Length 76; 87.5%; Pred. No. 2.2e+02; Live 2; Mismatches 0; Indels
Sequence 16, Application US/08503730

Patent No. 5780269

PATENT No. 5780269

APPLICANT: Inouye, Masayori

TITLE OF INVENTION: NEW HYBRID MOLECULES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weiser & Associates

STREET: 230 South Fifteenth Street Suite 500

CITY: Philadelphia

STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/503,730
FILING DATE: 18-JUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Weiser & Associates
230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
REGISTRATION NUMBER: 377(913).6277P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 07/817,430
FILING DATE: 06-7AN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              COUNTY: 05A

ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08507634 Patent No. 5849563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2165 gtcccaagccatcagc 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSE: Weiser &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-503-730-16
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                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                            APPLICANT: Miyata, Shohel
APPLICANT: Obshima, Atsushi
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: METHOD FOR SYNTHESIZING STABLE
TITLE OF INVENTION: SINGLE-STRANDED CDNA IN EUKARYOTES BY MEANS OF A BACTERIAL
TITLE OF INVENTION: RETRON, PRODUCTS AND USES THEREFOR
NUMBER OF SEQUENCES: 20
OCRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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bond to nucleotides 156-163 of SEQ ID NO: 11 of
this application."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide is linked to the 5' position of nucleotide number 1 of SEQ ID NO: 11 of this application."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The 2' position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION UNBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5584P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPHONE: 215-875-8394
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           Sequence 12, Application US/07753110B Patent No. 5436141 GENERAL INFORMATION:
                                                    20332 cecccaecccaecae 20316
           1457 cggcccagcccagcag 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2165 gtcccaagccatcagc 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_binding LOCATION: 69..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , CS-07-753-110B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                              :S-07-753-110B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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Human RAD50 Gene and Methods of Use Thereof 175\,
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0
                                                                                                                                                                                                                                                                                                                                                                                                    Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FILIPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 08/592,126
ATPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATPLICATION TREORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; L 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/08687080
Fatent No. 5965427
GENERAL INFORMATION:
TITLE OF INVENTION: Human RAD50 Gene and Met's CORRESPONDENCES: 175
CORRESPONDENCES: 175
GRESPER: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.
                                                                                                                 00786/345001
                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Scc.
100.0%; Pre
                                                 ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K. REGISTRAITON NUMBER: 38 615 REFERENCE/DOCKET NUMBER: 46 TELECOMMUNICATION INFORMATION:
                                                                                                           REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 70
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 gacagcaggtaccagc 1116
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 233 base pairs
nuclĕic acid
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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COMPUTER READABLE FORM:
                   APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 350 Camr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE:
US-08-717-294-93
                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 44
US-08-687-080-70
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                                                                                                                                                                                             TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This region can hydrogen
bond to nucleotides 156-163 of Si
this application."
                                                                     SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,634
FILING DATE: 25-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser Gerand J.
REGISTRATION NUMBER: 19,763
REFRENCE/DOCKET NUMBER: 377.6282P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 16; DB 2;
87.5%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE S.
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide is linked
nucleotide number 1
application."
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_binding
LOCATION: 69.76
OTHER INFORMATION: /note
OTHER INFORMATION: bond
CHER INFORMATION: this
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 76 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2165 gtcccaagccatcage 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 19
OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 176 Fe
CITY: Boston
STATE: MA
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Gaps

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APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Partick J.
APPLICANT: Sliver, Gary
APPLICANT: Sliver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
AUMBER OF SQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
    APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
HUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,069
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 16; DB
100.0%; Pred. No. 2.2
ive 0; Mismatches
                                                                                                                                                  ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 2618-17-
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: CANANTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                 CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-906-769-104/c
                                                                                                                                                                                                                                                 COUNTRY: U
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                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNDER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: INTRON 6 OF RAD50 GENOMIC SEQUENCE::3-08-687-080-70
                                                                                                                            Score 16; DB 2; Length 233;
Pred. No. 2.2e+02;
                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/630,822A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                   S-08-630-822A-97/c
Sequence 97, Application US/08630822A
Patent No. 5840695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "S-09:005-069-97/c
Sequence 97, Application US/09005069
Patent No. 5932470
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
                                                                                                                            Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (y 1478 aagaagtcagtaccca 1493
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TYPE: nucleic acid
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COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                       2 TTTGTGGTGGTAGAAT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 16; Conserv
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; 0

Length 252;

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Dale, Beverly
Stiegler, Gary
Stiegler, Gary
WENTION: USE OF PROTEASE INHIBITORS AND
WENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
WENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 3; Lv
Pred. No. 2.2e+02;
0; Mismatches 0;
RECIESTRATION NUMBER: 32,020
REFERENCE/DOOKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEFANCE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/817,795 FILING: DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 104, Application US/08817795
; Patent No. 6139840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rank, Glenn R.
Heath, Andrew W.
Tamaka, Miles Yamanaka
                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Scc.
100.0%; Pre
0;
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NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Rushlow, Keith E.
Hunter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1478 aagaagtcagtaccca 1493
                                                                                                                                                                                 LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.4
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: F US-08-906-616-104
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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STREET: 1/v.
CITY: Denver
STATE: Colorado
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                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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APPLICANT: Frank, Glen R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Score 16; DB 3; Length 252; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "At pos. bp 4, change A to R. At pos. aa 2, substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1700 Lincoln Street, Suite 3500
                                                                                                                                                             CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/906,616
05-AUG-1997
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OGTWARE: Patentin Pol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 104, Application US/08906616
Patent No. 6121035
GENERAL INFORMATION:
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Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ny 1478 aagaagtcagtaccca 1493
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AAGAAGTCAGTACCCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Sheridan 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..251
OTHER INFORMATION:
OTHER INFORMATION:
15-08-906-769-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :S-08-906-616-104/c
                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80203
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APPLICANT:
APPLICANT:
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0; Gaps

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FLEA PROTEASE PROTEINS
                                                                                                                                              Length 252
                                                                                                                                                                                    0; Indels
                                          /note= "At pos. bp 4, change A to R. At pos. aa 2, substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT F
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442A
                                                                                                                                            DB 3; L
                                                                                                                                         0.5%; Score 16; DB 100.0%; Pred. No. 2.2 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                        Application PC/TUS9514442A
                                                                                                                                                                                                                                                                                                                                                                                                          Grieve, Robert B.
Rushlow, Keith E.
Hunter, Shiriley Wu
Frank, Glenn R.
Heath, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gary J. Connell
REGISTATION UNDHER: 32,020
REFERENCE/FOCKET UNDHER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 865-9700
TELEFAX: (303 863-0223
INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              1478 aagaagtcagtaccca 1493
                                                                                                                                            Query Match 0.5%
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arfsten, Ann
Dale, Beverly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                    199 AAGAAGTCAGTACCCA 184
                     LOCATION: 1..251
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDALL
STREET: 1, CTTV: Denver
                                                                                                                                                                                                                                                                                                                                                     PCT-US95-14442A-104/C
                                                                                  US-08-639-075A-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION .
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                                                                                                                                                                                                                                                                                                                                                                          Length 252;
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATONNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPRATION POR SEO ID NO: 104:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 16; DB 3; I
100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
ITTLE OF INVENTION: FLEA PROTEASE PROTEINS, NU
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104, Application US/08639075A Patent No. 6150125 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         NAME/KEY: Xaa - any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
TELEPHONE: (303) 863-9700
TELEFAX: (303 863-0223
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1478 aagaagtcagtaccca 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 252 base pairs
nucleic acid
EDNESS: single
                                                                                      : 252 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AAGAAGTCAGTACCCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..251
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANDEDNESS:
                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-08-639-075A-104/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE
                                                                                                                                                                                                                                                                                          LOCATION:
"5-08-817-795-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                      LENGTH:
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Gaps
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                                                                                                                                                                   Non-A/Non-B/Non-C/Non-D/Non-E Hepatitis
Agents and Molecular Cloning Thereof
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/05980
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,986
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0201.49
TELECOMMUNICATION INFORMATION:
TELEFANE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        JUNESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
CONTAIN: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 16;
100.0%; Pred. No.
ive 0; Mismatc
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                                                  RESULT 53
PCT-US95-05980-98/c
; Sequence 99, Application PC/TUS9505980
; Sequence 99. Application PC/TUS9505980
; APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08937931
Patent No. 5935792
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rooke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ:
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 gccgcgagcggccgcg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 base pairs
                                                                                                                                                               TITLE OF INVENTION: Non-
TITLE OF INVENTION: Ager
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
 21 GCCGCGAGCGGCGCG 6
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GCCGCGAGCGGCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                    94306
                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-937-931-9
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GENERAL INFO
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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APPLICANT: Wages, John
APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Young, LaVonne
TITLE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No. 58
TITLE OF INVENTION: Agents and Molecular Cloning Thereof
NUMBER OF SEQUENCES: 106
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Length 252;
                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 2; Le
Pred. No. 2.2e+02;
0; Mismatches 0;
ore 16; DB 4; L
red. No. 2.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
 Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: US 025,396
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,493
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SCH Clone SU7-8
                                                                                                                                                                                                      Sequence 98, Application US/08611757 Patent No. 5859230 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Sccilarity 100.0%; Pr
Conservative 0;
Query Match

Best Local Similarity 100.0%; P

Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                              Kim, Jungsuh P.
                                                                       1478 aagaagtcagtaccca 1493
                                                                                                          199 AAGAAGTCAGTACCCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NO TITLE OF INVENTION: AG NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 350 Camr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94306
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ర
                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                           >,
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133 gccgcgagcggcgcg 148

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GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
TITLE OF INVENTION: Characterization of mRNA Patterns
TITLE OF INVENTION: in Neurites and Single Cells for Medical Diagnosis and
TITLE OF INVENTION: Therapeutics
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                             Length 489;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                               Score 16; DB 1; I
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                 0.5%; Scot. No. -
100.0%; Pred. No. -
0; Mismatches
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,131
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,254
FILING DATE: No. 595868ember 3, 1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US95/14792
FILING DATE: No. 595868ember 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jane Massey Licata, Esq. STREET: 210 Lake Drive East, Suite 201 CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: PENN-00219
TELECOMMUNICATION INFORMATION:
TELEFAN: (609) 779-2400
TELEFAN: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08848131 Patent No. 5958688
           TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                       1881 caggaaggggctgaga 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                               184 CAGGAAGGGGCTGAGA 199
                                                                                                                                                                                                                                                                                                               Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                    ESS: SINGLE
LINEAR
                                                                                                                                                      TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINEAR
                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08002
                                                                                                                                                                                                                      ; ANTI-SENSE:
US-08-334-254-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-848-131-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
TITLE OF INVENTION: USE OF NEURITE LOCALIZED MRNAS FOR
TITLE OF INVENTION: MEDICAL DIAGNOSIS AND THERAPEUTICS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Le . 2.2e+02;
              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,254
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jane Massey Licata, Esq. STREET: 210 Lake Drive East, Suite 201 CITY: Cherry Hill
                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: OSYAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: B97-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08334254 Patent No. 5723290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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75-08-937-931-9
                                                                                                                                                                                                                                                                                                                  FILING DATE:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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ZIP: 30303.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
US-08-507-016-8
                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Sequence 8, Application US/08507016
Sequence 8, Application US/08507016
GENERAL INFORMATION:
APPLICANT: EVANS, HELEN F.
APPLICANT: SHINE, JOHN
TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING
TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
                  ö
                    Gaps
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
ATILE OF INVENTION: USE OF NEURITE LOCALIZED MRNAS FOR
TITLE OF INVENTION: MEDICAL DIAGNOSIS AND THERAPEUTICS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; L. 2.2e+02;
  Pred. No. 2.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14792
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16;
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100.0%; Pre
0;
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                        1881 caggaaggggctgaga 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1881 caggaaggggctgaga 1896
                                                                               184 CAGGAAGGGGCTGAGA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
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                                                                                                                                                                             PCT-US95-14792-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 575;
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Sequence 4, Application PC/TUS9106418

GENERAL INFORMATION:

TITLE OF INVENTION: Antigens Associated with Polymyositi

TITLE OF INVENTION: and with Dermatomyositis

TITLE OF SEQUENCES: 14

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kilpatrick & Cody

STREET: 100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMPOTER: IBM PC Compatible
OPERATORS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; L 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,016
FILING DATE: 25-JULY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/108,733
FILING DATE: 03-SEP-1993
APPLICATION NUMBER: PCT/AU92/00097
FILING DATE: 06-MAR-1991
APPLICATION NUMBER: AU PK4953
FILING DATE: 06-MAR-1991
APPLICATION NUMBER: AU PK4953
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: .30,377
REFERENCE/DOCKET NUMBER: .30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06418
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (202)783*6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2400 aagcgggagctgcggc 2415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 16; Conservative
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0, 2.2e+02;
0; Indels
                                                                                                                                                                                                                  Length 609;
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Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOSS SOFTWARE: FASTER for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/911,319A
FILING DATE: August 14, 1997
PRICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MUMBER:
REGISTRATION NUMBER: 39,784
                                                                                                                                                                                                                    Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08911319A Patent No. 5968798
                                                                                                                                                                                                                  Query Match

Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
                                                                                        MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                       2740 gggccaggaggctgcc 2755
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             : 609 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                             564 GGGCCAGGAGGCTGCC 549
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
                                                                                                                                           163..609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLONE: 2447829
US-08-911-319A-2
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                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-338-579A-94
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-911-319A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                    TYPE:
                                                                                                           FEATURE
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Patent No. 606879.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gilliam, T. Conrad
APPLICANT: Tanzl, Rudolph E.
TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
TITLE OF INVENTION: DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: June 17, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; L
2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0575/44011-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 4; Pred. No. 2.260; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/579023
FILING DATE: 09-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: PADEL PALTERA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 278-04(
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                             TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    LENGTH: 578 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             955 ctggtgctgcttttgt 970
                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: N-termina
ORIGINAL SOURCE:
ORGANISM: Homo saplen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
19910905
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: JH2
TISSUE TYPE: Sera
                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSULT 60
S-08-338-579A-94/c
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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STREET: 700 Chesterfield Parkway No. 5824857th
                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,738
FILING DATE: 19920330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 GURRENT APPLICATION DATA:
PLICATION NUMBER: US/07/789,738
FILING DATE: 19920330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; L
Pred. No. 2.2e+02;
                                                                                                                                                                                            FILING DATE: 19920330
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: HOGHTET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10540)A
TELECHONE: (314)537-609
TELEFAX: (314)537-609
TELEFAX: (314)537-609
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 38-21(10540)A TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beachy, Roger N.
APPLICANT: Bhattacharyya, Maitrayee
TITLE BINATION: Plant Promoter
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 64
US-07-789-738-5
; Sequence 5, Application US/07789738
; Patent No. 5824857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19920330
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) US-07-789-738-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 714 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 GICCIGCACCACATCA 499
USA

61198

COMPUTER READABLE FORM:

MEDIUM TYPE: Flobre:

COMPUTER: Tree:

OPEPATER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  773 base pair
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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APPLICANT: Beachy, Roger N.
APPLICANT: Bhattacharya, Maitraye
TITLE OF INFORTON: Plant Promoter
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 5824857th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ' 0.5%; Score 16; DB 3; I 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CUSTURARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY DATE:

NAME: Muenzen, Colette C.

REGISTRATION WHBER: 39,784

REFERENCE/DOCKET NUMBER: PF-0363 US

TELEPHONICATION INFORMATION:

TELEPHONE: 550-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 654 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/911,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                    Sequence 2, Application US/09352619
Patent No. 6084070
GENERAL INFORMATION:
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101 GCGGGAGCTGCGGCAG 116
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: THP1NC
CLONE: 2447829
TS-09-352-619-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        94304
                                                                                                                                                                                                                                                                                                                                            CITY: Pa.
STATE: C.
COUNTRY:
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Sequence 128, Application US/08906769 Patent No. 6077687
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OTHER INFORMATION:
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OTHER INFORMATION:
US-08-906-769-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                    US-08-906-769-128/c
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                                                                                                                                                   Length 773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schulein, Martin
APPLICANT: Andersen, Lene N.
APPLICANT: Andersen, Soren F.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Lange, Lene
APPLICANT: Inare, Lene
APPLICANT: Inare, Michiko
APPLICANT: Inara, Michiko
APPLICANT: Taxaqi, Shinobu
IITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                   Score 16; DB 1; Le
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 3; Le
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT.
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
THE FOHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/08651136C
Patent No. 6001639
                                                                                                                                                 Query Match 0.5%; Sc
Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: '808 base pairs
TYPE: nucletc acid
STRANDEDNESS: single
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     1842 gtcctgcaccacatca 1857
                                                                                                                                                                                                                                                                                484 GICCIGCACCACATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear . MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 37..714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . LOCATION:
S-08-651-136C-15
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A to
56, G to V; at 457, A to M;
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460, A to R; at 470, G to S; at 493, A to R. A:
136, 152, 153, 154, 157 and 165, substitute Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Friedjer, Gary
APPLICANT: Sileqier, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FIEA PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: FIEA PROTEINS, NUCLEIC ACID
TITLE OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 16; DB 3; L
.00.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSFEICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24 APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 128, Application US/08906616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 865-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy 1478 aagaagtcagtaccca 1493
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Best Local Similarity 100.
Matches 16; Conservative
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US-08-906-616-128/c
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No. 60016390 No. 6001639disk of No. 6001639th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATONENTAL/AGERT INPOMMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/POCKET UNBER: 2618-25-C2
TELECOMMULCATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPRATION FOR SEO ID NO: 128:
SEQUENCE CHRARCTERISTICS:
LENTH: 815 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lange, Lene
APPLICANT: Nielsen, Ruby I.
APPLICANT: Ihara, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
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Pred. No. 2.2e+02;
MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 405 Lexington Avenue, 64th Floor
New York
                                                           ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York, COUNTRY: United States of America
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100.0%; Pre
0; /
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Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
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Best Local Similarity 100.0
Matches 16; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AAGAAGTCAGTACCCA 166
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                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.762
OTHER INFORMATION:
OTHER INFORMATION:
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: Colorado
RY: USA
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                                                                                                                                                             80203
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APPLICANT:
APPLICANT:
                                                                                                                                          COUNTRY:
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M; at 454, change G to V; at 456, G to V; at 457
460, A to R; at 470, G to S; at 493, A to R. At
136, 152, 153, 154, 157 and 165, substitute Xaa.
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                                                                          APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Patrick J.
APPLICANT: Slives, Patrick J.
APPLICANT: Slives, Patrick J.
APPLICANT: Slives, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 1990
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRAINON NUMBER: 32,020
REFERENCE/DOOKET NUMBER: 2618-25-C2-3
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              E: Sheridan Ross P.C.
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
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58-08-639-075A-128/c
Sequence 128, Application US/08639075A
Patent No. 6150125
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100.0%; Pre
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Rushlow, Keith E.
Wu Hunter, Shirley
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Stiegler, Gary
Gaines, Patrick J.
                                        Grieve, Robert B. Rushlow, Keith E.
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ADDRESSEE: Sheridan I
                                                                                                                                                                                                                                                                                                                                              ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION:
1.762
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
CTHER INFORMATION:
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STATE: Colorado
COUNTRY: USA
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APPLICANT: Grieve
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APPLICANT:
APPLICANT:
APPLICANT:
                                            APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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0.5%; Score 16; DB 3; Length 1048; 100.0%; Pred. No. 2.2e+02;
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 81, Application US/08933750C Patent No. 5932442
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Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555 TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bandman, Olga
Shah, Purvi
Au-Young, Janice
                                  INFORMATION FOR SEQ ID NO: 17 SEQUENCE CHRACKTESTRICS: LENGTH: 1048 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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13..906
                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                     linear
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JS-08-933-750C-81/c
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                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-651-136C-17
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Pred. No. 2.2e+02;
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CITY: New York
STATE: New York
STATE: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FTIING DATE: Z1-MAY-1996
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
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NUMBER OF SEQUENCES: 109
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4566.200-US
                                                                                                                AFFLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08651136C Patent No. 6001639
                                                                                                                                                             CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Lembiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAS: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lassen, Soren F.
Kauppinen, Markus S.
Lange, Lene
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 1031 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Lange, Lene
: Nielsen, Ruby I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Ihara, Michiko
: Takagi, Shinobu
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78-08-651-136C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Length 1225;
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US-08-739-485-4
; Sequence 4, Application US/08739485
; Sequence 4, Application US/08739485
; Sequence 6, Se63898
; GENERAL INFORMATION:
APPLICANT: Hillman Jennifer L.
APPLICANT: Banddman, Olga
TITLE OF INVENTION: NOVEL HUMAN LIM PROTEINS
NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                  0S-08-360-758-1/c

Sequence P, Application US/08360758

Patent No. 6074863
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Pathar, Shamkant A
APPLICANT: Egel-Mitani, Michi
APPLICANT: BOCCH, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PETELECOMMONICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1225 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
2168 ccaagccatcagcgtg 2183
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Clausen, Ib G
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                  928 CCAAGCCATCAGCGTG 913
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APPLICATION NUMBER:
FILING DATE:
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LIBRARY: Conc.
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IMMEDIATE SOURCE:
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                                                                                                         Length 1152;
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incuto
                                                                                                        DB 2; L6
2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
CUSTUARE: FastSEO for Windows Version 2.0
CUSTURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                      Query Match 0.5%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 16; Conservative 0; Mismatches
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PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18F058-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0356 US
                                                                                                                                                                                                                                                                                                       Sequence 81, Application US/09234613 Patent No. 6132973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                              2168 ccaagccatcagcgtg 2183
                                                                                                                                                                                                  928 CCAAGCCATCAGCGTG 913
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CLONE: 1602473
55-09-234-613-81
             LIBRARY: BLADNOT03
CLONE: 1602473
:S-08-933-750C-81
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 IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                      ::S-09-234-613-81/c
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ZIP: 94304
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Gaps

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DB 3; Length 1333; 2.2e+02;
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APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preett
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CSTURARE: FastSEG for Windows Version 2.0
CSTRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
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100.001
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; Sequence 9, Application US/09032372
; Patent No. 6008337
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                          NAME: Brook, David E.
REGIEGRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
                                                                                                                                        TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Diskette
IBM Compatible
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Best Local Similarity 100.
Matches 16; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM MEDIUM TYPE: Diskett
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58..840
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; LOCATION:
US-08-889-425-3
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APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
Algorian Algorian Algoromal-Associated Multispanning
TITLE OF INVENTION: Membrane Protein, LAPTM5 and a Nucleic Acid Encoding
TITLE OF INVENTION: LAPTM5
NUMBER OF SEQUENCES: GORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                               ADDRESSEE: No. 60748630 No. 6074863disk of No. 6074863th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                    SOFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,758
FILING DATE: 22-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800 105
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2.2e+02;
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                                                                                                                                                              COUNTRY: United States of America ZIP: 10174-6401
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6153403
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Best Local Similarity 100.0%; P

Matches 16; Conservative 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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REGISTRATION NUMBER: 33
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STATE: Massachusetts
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MEDIUM TYPE: Floppy
                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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TOPOLOGY: lir
MOLECULE TYPE:
US-08-785-396-7
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ADDRESSEE:
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                                                                                                                                                                  Length 1341;
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                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Preparation of Acariogenic Sugar TITLE OF INVENTION: Substitutes NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finnegan, Henderson, Farabow, Garrett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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2.2e+02;
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FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEYAGENT INFORMATION:
NAME: FORMAN, David S
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05638.0006-0
TELEPHONE: (202) 408-400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatcl
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Patent No. 5786140
                                                                                                                                                              0.5%; Scallarity 100.0%; Processive 0;
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STREET: 1300 I Street, N.W.
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
Kunz, Markwart
APPLICANT: Munir, Mohammed
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LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 16; Conserva
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Best Local Similarity
Matches 16; Conservi
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                                               TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT
CLONE: 2522306
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STATE: D.C
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594 GCTGAACCACTTCAGC 609

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O; Gaps
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                                                                                                                                                                TITLE OF INVENTION: Preparation of Acariogenic Sugar TITLE OF INVENTION: Substitutes NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takegi, Shinobu
APPLICANT: Boominathan, Karuppan C.
IILE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
CORRESPONDENCE ADDRESS:
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0. 2.2e+02;
0;
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ZIP: 2005-3315
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,396
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/374,155
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FORMAL, DAVIG S
REGISTRATION NUMBER: 33,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16;
Pred. No.
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; Sequence 1, Application US/08458023B
; Patent No. 5667990
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100.0%; Pro
Sequence 7, Application US/08785396
Patent No. 5985622
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                                                          APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
Kunz, Markwart
APPLICANT: Munir, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                  Washington
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                                           GENERAL INFORMATION:
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Sequence 4, Application US/08135510
Patent No. 5420028
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Conservative 0;
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NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1305 ACCCAGCACTIGGICC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1389 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1143 acccagcacttggtcc 1158
                                                                                                                                                                                                                                                                                                               FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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56679900 No. 5667990disk of No. 5667990th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Egel-Mitani, Michi
APPLICANT: Borch, Kim
APPLICANT: Clausen, Ib G
APPLICANT: Clausen, Mogens T
ITILE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1389;
                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-UN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 21,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; L6
2.2e+02;
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                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 80
TS-09-111-556A-1/C
Sequence 1, Application US/09111556A
Patent No. 6020180
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100.08; Pr.
0;
                   405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Candida antarctica
INDIVIDUAL ISOLATE: DSM 3855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pathar, Shamkant A
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 1389 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1143 acccagcacttggtcc 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to 1305 ACCCAGCACTTGGTCC 1290
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Best Local Similarity 100.
Matches 16; Conservative
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COMPUTER READABLE FORM:
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ADDRESSE: No. 60201
STREET: 405 Lexingto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Svendsel
APPLICANT: Pathari,
APPLICANT: Egel-Mi,
APPLICANT: BOrch, I
No.
                                                                                                 10174-6201
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          STREET: 400
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                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
5-08-458-023B-1
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Human Cholesterol
/lase, Method of Production and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                Length 1389;
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                              E: Foley & Lardner
3000 K Street, N.W., Suite 500
MBER: US/09/111,556A
22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Truncated Human
TITLE OF INVENTION: 7a-Hydroxylase,
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: JOYCE, JAMES G.
APPLICANT: GEORGE, HUGH A.
APPLICANT: HOFMANN, KATHRYN J.
APPLICANT: HOFMSEN, KATHRIN U.
APPLICANT: NEEPER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLLOMAVIRUS TYPE 18 VACCINE
                                                      GENERAL INFORMATION:
APPLICANT: CHIANG, John Young Ling
APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using It
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1524;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,953
FILING DATE: O7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
PRIOR APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/135,512
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT UNDER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT UNDER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT UNDER: 31,298
REFERENCE/COCKT NUMBER: 31,298
REFERENCE/COCKT NUMBER: 18748/219 HOCE
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; DB 1; L
No. 2.2e+02;
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                                                                                                                                                                                                                                   Foley & Lardner
00 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
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Patent No. 5820870;
GENERAL INFORMATION:
APPLICANT: GEORGE, HUGH A.
Sequence 4, Application US/08477953
Patent No. 5677159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 CAATCAAATATTTTC 237
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                ADDRESSEE: Foley
STREET: 3000 K S
CITY: Washington
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                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08483852
Patent No. 5650286
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using It
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
0.5%; Score 16; DB 1; Length 1524;
100.0%; Pred. No. 2.2e+02;
1ve 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
FILING DATE: 13-OCT-1993
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
FILING DATE: 13-OCT-1993
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
APPLICATION NUMBER: US 08/135,510
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET, NUMBER: 18748/220 HOCE
TELEPOMMUNICATION 'NFORMATION:
TELEPOMMUNICATION'
TELEPOMUNICATION'
TELEPOMMUNICATION'
TELEPOM
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; Pred. No. 2.20
0; Mismatches
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FILING DATE: 07-JUN-1995
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100.0%; Pre-
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TELEFAX: (204,)
TELEF : 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 caatcaaaatattttc 514
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Best Local Similarity 100.
Matches 16; Conservative
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
                                 Local Similarity
                                                                                                                                                                                                                                                                 SESULT 82
TS-08-483-852-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE:
   Query Match
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Matches
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APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using It
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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COMPUTER: IDPPY disk
COMPUTER: IDP PC compatible
OPERATING SYSTEM: R-DOS/MS-DOS
SPETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,952
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
PRIOR APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 16; DB 2; Lv 100.0%; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Folley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
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'APPLICATION NUMBER: US 08/135,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-477-952-4/c; Sequence 4, Application US/08477952; Patent No. 5851780
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                                                                                                                                                                    NAME: CARIY, CHRISTINE E
REGISTRATION NUMBER: 36,09
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION
TELEPHONE: 908-594-6734
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1524 base pairs TYPE: nucleic acid
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Best Local Similarity 100.
Matches 16; Conservative
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                TELEPHONE: 908-594-67
TELEFAX: 908-594-4720
                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                   APPLICATION NUMBER: FILING DATE: 22-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-408-669-1
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APPLICANT: JANSEN, KATHRIN U.
APPLICANT: JEPER, MICHAEL P.
ATILLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1524;
               ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 1; L
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,122
                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/408,669
FILING DATE: 22-MAR-1995
ATONNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08408669 Patent No. 5840306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION
TELEPHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISKETTE DISKETTE OPERATING SYSTEM: DOS SOFTWARE: FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 cctgcaggtggtggca 242
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                            ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UR-08-409-122-1
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Gaps
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     Length 1713;
                                                                                                                                                                                                                                                                                                                                                  BACTERIAL CATABOLISM OF CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                    E: FISH & RICHARDSON P.C. 4225 Executive Square, Suite 1400
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,452A
FILLING DATE: 13-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          RESULT 88
US-08-600-452A-5/c
; Sequence 5, Application US/08600452A
; Patent No. 5985644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08467948A Patent No. 5998164
     Ouery Match 0.5%; Somest Local Similarity 100.0%; P. Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 071
                                                                                                                                                                                                                                                                                            APPLICANT: CHITLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-600-452A-5
                                                                                                                                                                                                                                                                                  KEYHANI, NEMAT O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (619) 678-5070
(619) 678-5099
                                                                                                                                                                                                                                                ROSEMAN, SAUL
BASSLER, BONNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176 tcagttcacaaccttc 1191
                                                                       1176 tcagttcacaaccttc 1191
                                                                                         241 TCAGTTCACAACCTTC 226
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Best Local Similarity 100.
Matches 16; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LI, YI
APPLICANT: CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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STREET: 422
TTTY: La JOlla
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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n. 2.2e+02;
0; Indels
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APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAY
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4130/206916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  0.5%; Scc.
100.0%; Pre
0;
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 1874(
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFRX: (202)672-5309
TELEFX: 904136
INFORMATION FOR EQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HOBES, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130,
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'S-08-386-727-5/c
Sequence 5, Application US/08386727
Patent No. 5792647
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
.S-08-386-727-5
                                                                                                                                                                          LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 16; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                linear
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20005
                                                                                                                                                                                                                            TOPOLOGY:
TS-08-477-952-4
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APPLICANT:
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: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET.
CHICAGO
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-467-947A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein IIILE OF INVENTION: Coupled Receptor GPR2 NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein IITLE OF INVENTION: Coupled Receptor GPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1713;
                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                          COUNTRA.

ZIP: 20005
COMPUTER: PLOPEN:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COPPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
TITING DATE: 06-10N-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.114000:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                    GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08467947A Patent No. 6090575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NI, JIAN
GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRAN
ROSEN, CRAIG A.
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Best Local Similarity 100.
Matches 16; Conservative
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116..1003
                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: STERNE, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIF
APPLICANT: NI, JIAN
APPLICANT: GENTZ, F
APPLICANT: SULT, CA
APPLICANT: SULT, CA
APPLICANT: SULT, CA
APPLICANT: SULT, CA
APPLICANT: SULTON I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: bo
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74-08-467-948A-1
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Sequence 13, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: DCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEPEF, ERIC K.
REGISTRATION NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
TELEPHONE: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two First National Plaza, 20 South Clark STREET: Street
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 16; DB 3; I
100.0%; Pred. No. 2.3e+02;
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RESULT 93
US-09-146-249A-13
US-09-146-249A-13
Sequence 13, Application US/09146249A
Patent No. 6062240
GENERAL INFORMATION:
APPLICANT: Wighler, Michael H.
APPLICANT: Colicelli, John J.
ITILE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
STREET: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Illinois
CONTY: Chicago Sars Tower, 233 South Wacker Drive
CITY: Chicago STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPTER: IBM PC compatible
COMPUTER: IBM PC Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1721;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 16; DB 2; I
100.0%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEKA 312-474-0448
TELEK: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERICS:
LENGTH: 1721 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2731 cacagccgcgggccag 2746
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 16; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          ), NAME/KEY: CDS
; LOCATION: 66..1274
US-08-474-379C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: .66..1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECUPE TYPE: CDNA
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-146-249A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
CITY: Chicago
STREET: 111nois
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 19-MAR-1994
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1721;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEFRA: (312) 984-9740
TELEFRA: (312) 984-9740
TELEFRA: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5-08-474-379C-13
Sequence 13, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
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LOCATION: 60..1274
::S-07-688-352C-13
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MOLECULE TYPE: cDNA
FEATURE:
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0.5%; Scc...
100.0%; Pre
0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Blogen, Inc.
STREET: 14 Cambridge Center
CITY:.,Cambridge
STATE: Massedusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1721 base pairs
NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                        Gaps
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APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1721;
 Length 1721;
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                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-AMR-1994
CLASSIFICATION BATA:
PRIOR APPLICATION DATA:
DB 3; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 16; DB 3; L
.00.0%; Pred. No. 2.3e+02;
0.5%; Score 16; DB 100.0%; Pred. No. 2.3 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSULT 95
CT-US91-02714-13
Sequence 13, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
                                                                                                                                                                                                       Sequence 13, Application US/08206188B Patent No. 6100025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2731 cacageegeggeeag 2746
                                                                             2731 cacageegeggeeag 2746
 Query Match
Best Local Similarity 100.C
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                266 CACAGCCGCGGGCCAG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66..1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
-3-08-206-188B-13
                                                                                                                                                                                   3-08-206-188B-13
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Gaps
APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 96
US-08-481-814A-2
; Sequence 2, Application US/08481814A
; Patent No. 5869040
; GENERAL INFORMATION:
APPLICANT: Hsu, Yen-Ming
: TITLE OF INVENTION: GENE THERAPY METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19910419
CLASSIFICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
ATONINY/AGENT INFORMATION:
NAME: BOLUN, MICHAEL S.
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
REFERENCE/COCKET NUMBER: 25467
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 4; Lv
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                      Length 1790;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                          Score 16; DB 2; L
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SUSTWARRE: FastsEO for Windows Version 2.0
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,529
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 98
US-09-231-529-2
; Sequence 2, Application US/09231529
; Patent No. 6096308
; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/977,816
               REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1790 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELECHONE: 650-855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTAL.
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: DOSPATIBLE
MEDIUM TYPE: DOSPATIBLE
MEDIUM TYPE: DOSPATIBLE
MEDIUM TYPE: DOSPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                1581 tctctgctactggact 1596
                                                                                                                                                                                                                                                                                                                                                                     1235 TCTCTGCTACTGGACT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
                                                                                                                                                                                                                                                                          Ouery Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3174 Porter Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650-845-4166
                                                                                                                                               nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIDNNOT25
                                                                                                                                                                                                        CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: KIDNN
; CLONE: 3453694
US-09-231-529-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                   ; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-993-228-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,814A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 429..1739
CHER INFORMATION: /product= "E2F-2"
S-08-481-814A-2
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Scur
100.0%; Prr
0;
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Patent No. 5976838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KAPLAN, WALTER A
REFERENCE/DOCKET NUMBER: A00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2000
TELEFAX: 617-679-2000
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       1766 base pairs
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                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics
STREET: 87 Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Jacobs,
APPLICANT: MCCOY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
MOLECULE TYPE: HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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0.5%; Score 16; DB 1; Let 100.0%; Pred. No. 2.3e+02;
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Job time: 24889 sec
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100.001
100.001
                                                                               ATTORNEY AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2069 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1298 AGATTTGGCTGAAGA 1313
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 16; Conserve
                                                                                                                                                                                                                                                                                                                                                     linear
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0.5%; Score 16; DB 3; Length 1977;
100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SMADI EXPRESSION
CURRENT APPLICATION NUMBER: US/09/255,911
CURRENT APPLICATION NUMBER: 1999-02-23
NUMBER OF SEQ ID NOS: 46
LENGTH: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FOOR, FOITEST
APPLICANT: KAHN, Jennifer,
APPLICANT: KAHN, Jennifer,
APPLICANT: KAHN, Jennifer, - PARENT, S.A.
APPLICANT: WARRINAN Jean, - RAMADAN, N.M.
APPLICANT: WARRINAN, Nancy, - REGISTER, E.A
APPLICANT: ONISHI, Janet, - SHEI, Gan-Ju
TITLE OF INVENTION: SYNTHASE SUBUNITS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: JOSEPH A. COPPOLA - MERCK & CO., INC
126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Le
2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/619,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEMAS, Joseph
EL-SHERBEINI, Mohammed
                                                                                                                                                                                                                              Sequence 1, Application US/09255911
Patent No. 6013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08619554 Patent No. 5821353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Diskette
IBM Compatible
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                                                                                     1462 cagccccagcagagaa 1477
      Query Match 0.5%
Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                            419 CAGCCCCAGCAGAA 434
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESS: JOSEPH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (433)..(1830)
3-09-255-911-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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Length 2069;

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em_esthum6:*
em_esthum7:*
em_esthum8:*
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em_esthum11:
em_esthum12:
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em_esthum17:
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em_estin1:*
em_estin2:*
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em_estom2:
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em_estin4:
em_estov1:
em_estov2:
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em_estro4:
em_estro5:
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em_estpl2
em_estpl3
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em_estp15:
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9b_est44:
9b_est46:
9b_est46:
9b_est48:
9b_est49:
9b_est50:
9b_est51:
9b_est51:
9b_est51:
9b_est51:
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gb_est42:
                                                                       February 18, 2001, 05:22:53; Search time 2148.29 Seconds (without alignments) 9648.673 Million cell updates/sec
                                                                                                                                                            1 cgcgggcgtaggtgaccggc.....aataaagattgagtttgcaa 2958
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                           7991742 seqs, 3503743858 residues
                                                                                                                                                                                                                                                                              otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 Sost-processing: Listing first 100 summaries
                                                 .M nucleic - nucleic search, using sw model
                                                                                                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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2958
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em_estfun:
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Perfect score:
Requence:
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em_estro14:*
em_estro15:*
em_estro16:*
em_estro17:*
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9D_est58:*

9D_est50:*

9D_est60:*

9D_est61:*

9D_est61:*

9D_est62:*

9D_est64:*

9D_est66:*

9D_est66:*

9D_est77:*

9D_est77:*

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gb_gss24:
gb_gss24:
em_gss14:
em_gss15:
em_gss15:
em_gss17:
em_gss17:
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9D-est82:
9D-est843:
9D-est843:
9D-est85:
9D-est86:
9D-9SS1:
9D-9SS2:
9D-9SS2:
9D-9SS2:
9D-9SS3:
9D-9
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190: gb_gss25:* 191: gb_gss26:* 192: gb_gss27:* 193: gb_gss28:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES t Query Conto Match Length DR ID	1 676 22.9 676 106 BE260495 BE260495 60115070	614 20.8 975 105 BE250412 BE250412 600943. 590 19.9 664 107 BE383336 BE38338 601298	590 19.9 692 107 BE382353 BE382353 60129865	537 18.2 627 107 BE386924 BE386924 60127481 528 17.8 761 135 BE795820 BE795820 60159085	521 17.6 688 135 BE794311 BE794311 60159144	8 478 16.2 531 92 AW572950 AW572950 hII7h05.	45 15.5 531 4 AA243700 AA243700 zr68g08.s	1 451 15.2 451 17 AI200296 AI200296 gf86b12 2 450 15.2 812 136 BE867512 BE867512 601443	3 448 15.1 499 91 AW510825 AW510825 AW510825 AW510825 AW510825	4 447 15.1 938 106 BE260626 BE260626 60114 5 447 14.0 403 02 200575677	6 438 14.8 612 106 BE304720 BE304720 60110	17 436 14.7 493 7 AA455121 AA455121 ZX/8CU4	425 14.4 527 16 AI089646 AI089646 qb16g07.	0 421 14.2 421 20 A1468143 A1468143 tf92 1 421 14.2 536 87 AW206103 AW206103 UI-H	2 404 13.7 404 88 AW304130 AW304130 xs13e05.	3 4U2 13.5 4/4 4 AAZY16/U AAZY16/U 2L3/UU4: 4 400 13.5 992 135 BE747163 BE747163 601577	5 384 13.0 574 105 BE250309 BE250309 60094345 6 380 12.8 431 5 AA310236	949 135 BE744197 6015771 370 137 BE83516 6015080	9 368 12.4 745 137 BE900936 BE900936 60167420	0 352 11.9 518 144 R87541 R87541 R87541 ym89b04.r 1 351 11.9 855 146 W27286 W27286 28h1 Huma	32 347 11.7 790 137 BE892893 BE892893 6014357	3 343 11.6 396 12 AABII170 AABII170 OD42CU3. 4 342 11.6 446 10 AA634909 AA634909 AD27h02.	5 342 11.6 452 10 AA679618 AA679618 ag72c12 6 341 11.5 698 135 BE795434 . BE795434 601592	7 338 11.4 345 90 AW407520 AW407520 UI-HF-BM0	9 330 11.2 416 106 BE298273 BE298273 6011181	0 329 11.1 940 135 BE/43831 BE/43831 bE/43831 0U15///4 1 325 11.0 531 27 A1937465 A	42 323 10.9 397 10 AA632118 AA632118 np66h03.	4 315 10.6 366 4 AA233087 AA233087 Zr68g08.r	5 307 10.4 735 137 BE902696 BE902696 6016773	47 301 10.2 480 144 R90875 R90875 Yn01d02.r	301 10.2 511 95 AW771657 AM771657 hn59 291 9.8 297 97 AW994476 AW994476 RC3-	50 291 9.8 404 17 AII74501 AII74501 and 2e05.s	1 290 9.8 494 136 BE858252 792 2 287 9.7 414 105 BE243887 BE243887 TCB	3 286 9.7 355 6 AA353573 AA353573 EST61719	5 284 9.6 394 88 AW248468 AW248468 2820540	56 283 9.6 489 25 AI803400 AI803400 tc42103.7 57 282 9.5 307 145 T34216 T34216 EST64346.	8 281 9.5 489 8 AA534478 AA534478 nf76f10.s
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FEATURES	BASE COUNT 154 a	Query Match Best Local Similari Matches 676; Cons	Oy 1143 acccagcactt	Db 61 ATTCAAACCCA Qy 1263 tgtaagaagga Db 121 TGTAAGAAGGA	Oy 1323 taccagctccg
AA635046 ab48b06.r AA994126 ou38b06.s BE744876 601576324 AI033108 ow99908.s AM59223 hf41a01.x AM59223 bf41a01.x AA311855 EST182568 Z17886 HSDHEIO30 AI991599 ws18c04.x BE938229 CM4-TNO06 AA838624 oe91f04.s AW889463 RC6-NIO02 HE409312 60130040	AI201492 qs74b03.x AF188525 AF188525 H14462 yl25f04.rl AAS22537 h138e08.s	A492808 OM/3503.5 T34024 EST61387 Hu AI357786 qu98807.x BE615669 601279347	AA235532 zt2911.s A1804749 tu42d02.x AW296524 UI-H-BW0- N36229 YY30c04.s1 AW511765 xu70f03.x AW511765 xu70f03.x	AM3/824/ KCI HTUZI AM3/04146 aa59e06.s W3/591 zc10f03.r1 R51138 yg71c08.r1 AI141263 qa46h05.s AM3/6268 R555407	A43 8424 E190920 244544 HSC22E061 n H03318 yj47e10.s1 A1033342 0x02d12.s BE619874 601473130 T72963 yc65b06.r1
276 9.3 461 10 AA635046 273 9.3 364 87 AW175581 266 9.0 984 13 BE744876 255 8.6 410 15 AT031108 255 8.6 461 92 AW59223 253 8.6 461 92 AW59223 250 8.5 501 5 AW31185 247 8.4 299 147 Z1786 247 8.4 517 27 AT991599 246 8.3 329 12 AA838624 243 8.2 346 96 AW88463 243 8.2 346 96 AW88463 236 8.0 691 107 BE409312	7.9 439 17 A 7.9 233 14 A 7.9 294 141 A 7.8 865 8 A 7.7	7.7 282 1 7.7 282 1 7.7 4433 1 7.6 872 1	7.5 291 4 A 7.4 228 88 7.4 448 142 7.2 316 91 7.1 249 88	209 7.1 650 89 AW3/824/ 207 7.0 219 8 AB504146 206 7.0 422 146 W37591 199 6.7 472 144 R51138 198 6.7 416 16 AI141263 193 6.5 394 6 AAB46268	6.2 290 147 6.2 290 147 6.2 424 141 6.1 482 15 6.1 577 110
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ALIGNMENTS

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72260495
BE260495
BE260495
G01150702F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503184 5',
mRNA Sequence.
BE260495.1 G1:9131807
EEST
BEACO SECT
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Location/Qualifiers 1. 676 /organism="Homo sapiens" /db_xxef="taxon:9606" /clone="IMAGE:393184" /clone="IMAGE:393184" /tissue_type="neuroblastoma" /tissue_type="neuroblastoma" /tab_host="bH10B (phage-resistant)" /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies). Note: this is a NIH MGC Library."	15	<pre>atch 22.9%; Score 676; DB 106; Length 676; al Similarity 100.0%; Pred. No. 0; 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	acccagcacttggtcctgaatgagaactgtgcctcagttcacaaccttcgcagccacaag 1202 	attcaaaccoagotcaacctcatccaccggacatcttcccctgctcaccagtttccgc 1252	tgtaagaaggaggccccaccctcagtgtgcccatggttcagggtgaatgcctcctcaag 1322 	taccagctccgtcccaggagggagtggcagagggatgccattattacttgcaatcctgag 1382 	gaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtgcaggagtacagg 1442 	aggagtgcgcaggaccagcccagcagagaaaagaagtcagtacccagaaatcatc 1502 	ttoottggaacagggtotgccatcccgatgaagattcgaaatgtcagtgccacacttgtc 1562 	aacataagccccgacacgtctctgctactggactgtggtgagggcacatttgggcagctg 1622 	tgccgtcattacggagaccaggtggacagggtcctgggcaccctggctgctgttttgtg 1682 	teceacetgeacgeagteaceacaegggettgecaagtatettgetgeagagaaege 1742 	gccttggcatctttgggaaagccgcttcacctttgctggtggttgccccaaccagctc 1802 	aaagcctggttccagc 1818
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Thu Feb 22 15:01:09 2001

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Query Match
Best Local Similarity
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                                                       A EST 13-JUL-2000 sapiens cDNA clone IMAGE:2960077 3'
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 975)
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/clone_lib="NIH_MGC_17"
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100.0%; Pred. No. v,
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/db_xref="taxon:9606"
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High quality sequence stop: 756
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TITLE
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/note="Organ: brain; Vector: POTB7; Site_1: XhOI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/AhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 664)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE383336 664 bp mRNA EST 21-JUL-2000 601298249F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628308 5'
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                                                                                                                                                                                                                 tgaagagcacggtcccccaggaggcagctcaggataggtggtagtggggctgtgccgaggc
                                                                                          aggetgtgtgtettetgeeceaegeaegeaecegtatetgeeeteettgetggtagaage
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/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:3628308"
/clone=lib="NIH_MGC_19"
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Location/Qualifiers
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Length Indels

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/tissue_type="neuroblastoma"
//lab_host="DHIOB (phage=resistant)"
//lab_host="DHIOB (phage=resistant)"
//lab_host="Orden: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; CDNA made by Oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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601274815F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:3615939 3
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                            /clone="IMAGE:3629028"
/clone_lib="NIH_MGC_19"
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC Clone distribution information can.be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl,ggov. Plate: LLCM314 row: o column: 13
High quality sequence stop: 600.
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Tel: (301) 496-1550
Emall: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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/lab_host="DHIOB (phage-resistant)
/nab_host="DHIOB (phage-resistant)
/note="Organ: skin; Vector: poTB7; Site_1: Xho!; Site_2:
/note="Organ: skin; Vector: poTB7; Site_1: Xho!; Site_2:
/note cond into EcoRIXho! sites using the following 5'
adaptor: GGCACGAG(6): Size_resiected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM280 row: n column: 04
High quality sequence start: 18
High quality sequence stop: 611.
Location/Qualifiers
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_20"
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/note="Organ: lung; Vector: porBT; site_1: xhoI; site_2: EcoRI; cDNA made by oliqo-dT priming. Directionally aloned into EcoRI/KhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong In the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammallan Gene Collection (MGC)
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.2e-268;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
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/clone="IMAGE:3945085"
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/clone="lib="NIH_MGC_7"
/tlssue_type="small cell carcinoma"
/tell_line="MGG3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung: Vector: poTP7; Site_1: XhoI; Site_2: ECORI, cDNA made by oliqo-dT priming. Directionally ECORI; cDNA made by oliqo-dT priming. Directionally clong into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Joses 1 to 688)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Bmail: Robert_Strausbergenih.gov

Tissue Robert_Strausbergenih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory,

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Theyte Genomics, Inc.

Clone distribution: MGC clone distribution information can:be
found through the I.M.A.G.E. Consortium/LLNL at: image.linl:gov

High quality sequence stop: 688.
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                           241 TCACCCTTTGCTGGTTGCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAA
                                                                                        301 CCAGTGCCAGGAGGTCCTGCACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGG
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/clone="IMAGE:3945538"
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insert'size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Pred. No. 2.1e-264;
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                                                                                                                                                                                                                                                                                  /note="Organ: pooled; Vector: p1713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I:M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Soares and M. Fatima Bonaldo. "
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                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco High quality sequence stop: 459.
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                                                                                                                                                                                                                           /clone="IMAGE:2932185"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                    Location/Qualifiers
Unpublished (1997)
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SCOL

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Examples Searyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 823)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausbergenih.gov

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The CDNO distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

http://image.llnl.gov

Righ quality Sequence Stop: 695.
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/fissue_type="large_cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oliço dI.
Site_2: Insert size 1.8 kb. Library constructed by Life
Technologies.
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BEG19259 823 bp mRNA EST 24-AUG-2000 601473130F1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3876223 :
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/db_xref="taxon:9606"
/clone="IMAGE:3876223"
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                                                                                                                                                                                                                                                                                                    AA243700 531 bp mrna EST 07-MAR-1997 zr68908.s1 Scares.NhHWDLS1 HOMO sapiens cDNa clone IMAGE:668606 3' similar to SW:XK50_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2_MTD1 INTERGENIC REGION. ;, mrna sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 531)
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/clone_llb="Soares_NhiMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 466.

Location/Qualifiers
1. 531
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435 ATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCCACCCTCC 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity 100.0%; Pred. No. 5e-231;
Matches 458; Conservative 0; Mismatches 0; Indels
                                                         /organism="Homo sapiens"
/db_xref="GDB:5562573"
/db_xref="taxon:9606"
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Tumor Gene Index

U Dpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
This clone is available royalty_free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Up from Gibco
High quality sequence stop: 442.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

/db_xref="Homo sapiens"
/db_xref="Haxon:9606"
/clone="InhaGE:1756895"
/clone="InhaGE:1756895"
/dev_stage="19 weeks"
/dev_stage="19 weeks"
/dev_stage="10 weeks"
/dev_stages"
/dev_stage="10 weeks"
/dev_stages"
/dev_stages"
/dev_stages"
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IMAGE:1756895 3' similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. ;, mRNA sequence.
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
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AI200296.1 GI:3752902
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/clone_"IMAGE:3847226"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/tlab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORI6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo GI.
Average insert size 1.8 kb. Library constructed by Life
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Pational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Pumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                      61 ATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAGGACGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014 gagaatgccacctttcagaggtaccaaggaaaggcagatgcccccgtggccttggtggtt
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                                                                                                                                                                                                                                                                                                      1 GCTTTCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAGGAG
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                                                                                                                                                                                                    Score 450; DB 136;
Pred. No. 9e-227;
0; Mismatches 0;
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                                                                                                                        Technologies.
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AW510825.1 GI:7148903
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                                                                                                                                      216 c
                                                                                                                                                                                                       Query Match 15.2
Best Local Similarity 99.8
Matches 570; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 812)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@Enih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEB67512 812 bp mRNA EST 27-SEP-2000 601443010F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847226 5', BE867512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inco.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 686.
Location/Qualifiers
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0
                                                                    Length 451;
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                                                                    15.2%; Score 451; DB 17; Lilarity 100.0%; Pred. No. 2.6e-227; Conservative 0; Mismatches 0;
     93
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/db_xref="taxon:9606"
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SSULT 12 S867512 COCUS

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SEFERENCE AUTHORS TITLE JOURNAL

TATURES

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BE260626.1 GI:9132065
                                           mRNA sequence.
BE260626
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AUTHORS
TITLE
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                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2460 gaggatggggagcetcagcagaagcgggcccacacagaggccacagggccaagagtc 2519
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                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone="IMAGE:2911965"
/clone_lib="Soares_NFL_T_GBC_S1"
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                           High quality sequence stop: 470.
Location/Qualifiers
                                                                                                                                                                                                                         'lab_host-"DH10B'
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Best Local 9
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L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-155
Tel: (301) 496-155
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium/LINL at: image.linl.gov
Plate: LLCM19 row: o column: 04
High quality Sequence Stop: 621.
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                                                                                                                                                                                                              Homo sapiens
Veraryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
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BE260626 938 bp mRNA EST 13-JUL-2000 601146116F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161691 5'
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
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Similarity 100.0%; Pred. No. 3.5e-225;
17; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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500

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Q Þ SFINITION

:SSULT 1: :W575677

CCESSION ERSION EYWORDS

ORGANISM

OURCE

AUTHORS TITLE JOURNAL

SFERENCE

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/tissue_type="adenocarcinoma cell line"
/lab_host="NH10B (phage-resistant)"
/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG(). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
178 c 161 g 130 t
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 612)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert. Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert. Strausberg@nih.gov

Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM143 row: h column: 09
High quality sequence start: 21
High quality sequence stop: 609.
Location/Qualifiers
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121 GGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGC 180
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_15"
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/clone=IMAGES:3061957"
/clone=Inb="NHIMGC_38"
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/cell_line="MGC85"
/lab_host="multo" (LTI)"
/lab_host="multo" (LTI)"
/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT773-Pac; Site_1: NotI; Site_1: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. Tissue Procurement: Louis M.
Staudt, M.D., Ph.D.
CDN Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: M.C. clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
POLYA-NO.
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NIH-WGC http://www.nobi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                       141 cggccgcgcaaggacccgctgcggcacctgcgcacgcgagagaagcgcggaccgtcgggg 200
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99.8%; Pred. No. 1.5e-222;
ative 0; Mismatches 1;
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/db_xref="taxon:9606"
                                                                                                                                                                1412
                                                                                                                                                            Location/Qualifiers
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AW575677.1 GI:7247216
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I (Dases 1 to 493)

Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterstron,R. and Wilson,R.

WashU-Merck EST Project 1997

Unpublished (1997)

Contact: Wilson RK
WashIngton University School of Medicine
MashIngton University School of Medicine
Tel: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llni.gov) for further information.

Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Seq primer: -41ml3 fwd. ET from Amersham

High quality sequence stop: 100 Mersham

High quality sequence stop: 100 Mersham
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LUMOY NDHOT HOMO SADJEDS CDNA CLONE
tO SW.YKS9_YEAST P36159 HYPOTHERICAL 96.8
INTERGENIC REGION, ;, mRNA SEQUENCE.
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                                                          ctcatccacccggacatcttccccctgctcaccagtttccgctgtaagaaggagggccc 1280
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Length 612;
                               Indels
tch 14.8%; Score 438; DB 106; al Similarity 100.0%; Pred. No. 2e-220; 438; Conservative 0; Mismatches 0;
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zx78c04.sl Soares ovary tu
IMAGE:809862 3' similar to
KD PROTEIN IN SIS2-MTD1 IN
AA455121 GI:2177897
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/Lissue_type="ovarian tumor"
/Lisbue_type="ovarian tumor"
/Lisb_host="DH10B (ampicillin resistant)"
/Lisb_host="DH10B (ampicillin resistant)"
/Lisb_host="DH10B (ampicillin recipillin reci
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xref="GDB s639680"
/db_xref="taxon:9666"
/clone="IMAGE:809862"
/clone_lib="Soares ovary tumor
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NoTI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergehih.gov
Famil: Robert Strausbergehih.gov
Famil: Robert Strausbergehih.gov
Famil: Robert Strausbergehih.gov
Fuls clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 463.

Location/Qualifiers

II : 577

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/clone="IMAGE:1696476"
/clone="IMAGE:1696476"
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Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 527)
        IMAGE:1696476 3', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female'
                                                                         SOURCE
ORGANISM
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                                                                                           th LLNL; contact the further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2843 ccagcaaagtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaa 2902
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Tumor Gene inue.

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LJ
IMAGE Consortium (info@image.llnl.gov) for fur
Seq primer: -40Up from Gibco
High quality sequence stop: 451.

Location/Qualifiers
                                                                                                                                                                                                                                            /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.4%; Score 425; DB 92; 99.8%; Pred. No. 1.5e-213; ative 0; Mismatches 1;
                                                                                                                                                                                             /organism="Homo sapiens"
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14.4%; Score 425; DB 16; Length 527;
Best Local Similarity 99.6%; Pred. No. 1.5e-213;
Matches 525; Conservative 0; Mismatches 2; Indels (
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conA Library Arrayed by: Greg Lennon, Ph.D.

conA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing by: Washington Cone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/Dbrp/Image/Image.html
Insert Length: 733 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers
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                                                                                                                                                                                                tf92g05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2106776 3' similar to SW:XX59_YEAST P36159 HYPOTHETICAL 96.8 KD PROFEIN IN SIS2-MID1 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      issue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFIGAP), Tumor Gene Index
                 2850 agtgattccctgcacaccagagacaagcagagtaacaggatcagggtcagtgggtctaagtgtccg 2909
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                                   107 AGTGATTCCCTGCACCACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCG 48
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/lab_host="DH108"
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100.0%; Pred. No. 2e-211;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
1301) 496-1550
Email: Robert_Strausberg@nih.gov
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1. 536
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2723471"
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/clone="IMAGE:2723471"
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/note="Vector: pT773D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECG RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub3 library; which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP_LOSO
// NCI_CGAP_PT22, NCI_CGAP_PT28, NCI_CGAP_COSO
// NCI_CGAP_PT22, NCI_CGAP_RIG1; NCI_CGAP_LOSO
// NCI_CGAP_RIG3, NCI_CGAP_RIG1; NCI_CGAP_LOSO
// NCI_CGAP_BT2, NCI_CGAP_LUS5, NCI_CGAP_LUS4,
// NCI_CGAP_BT2, NCI_CGAP_LUS5, NCI_CGAP_LU24,
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Tel: (301) 496-1550
Bmail: Robert_Strausbergenih.gov
Oligo-dr track not found. Not I site shown in beginning of sequence
oligo-dr track not found. Not I site shown in beginning of sequence
is likely interpal to the message. cDNA Library Preparation: M.B.
Soares Lab Coine distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW206103 536 bp mRNA EST 02-DEC-1999 UI-H-BII-afx-f-12-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723471 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 gggegecgegetetaegtetteteegagtteaaceggtatetetteaactgtggagaagg
                                                                                                                                                      320 cgttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaacatattcct
                                                                                                                                                                                                                                                                                                                380 gacacgaatgcactggtctaatgttgggggcttaagtggaatgattcttactttaaagga
                                                                                                                                                                                                                                                                                                                                                                                         241 GACACGAATGCACTGGTCTAATGTTGGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGA
                                                                             121 GGGCGCCGCCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAAGG
                                                                                                                                                                                                                                   181 CGTTCAGAGACTCATGCAGGAGCACAAGTTAAAAGGTTGCTCGCCTGGACACATATTCCT
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Email: Robert_Strausberg@inh.gov
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Lorary Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clond Stribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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           AW304130.1 GI:6713819
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Unpublished (1997)
                                                                                                                           Homo sapiens
                                                                                        human.
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NCI_CGAP_Lu19, NCI_CGAP_GC6,

NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,

Single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LiAM 334-337, 3862-3863,

NCI_CGAP_Kid3 pool 1 LiAM 334-337, 1456008-1456775, 1500552-150285); NCI_CGAP_Kid5 pool 1 LiAM 338-3342, 376-3785, 376-3786 [IMAGE CloneIDS 1323912-132581, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LiAM 3575-3582, 3851-3854 [IMAGE CloneIDS 1329912-128581, 1520904-1522439); NCI_CGAP_GC4 pool 1 LiAM 3164-3167, 3716-3720, 373-3735 [IMAGE CloneIDS 127096-128681, 1469064-1470983, 1475592-1476743); NCI_CGAP_CC10 pool 1 LiAM 2457-2459, 2758-2759, 3062-3068 [IMAGE CloneIDS 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_CC10 pool 1 LiAM 2644-145351). Subtraction was performed as previously described [Bonaldo, Lenon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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Pred. No. 2e-211;
0; Mismatches 1;
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TAG_TISSUE=lung
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143 c
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Best Local Similarity 99.8%;
Matches 471; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InMAGE:2769566"
/clone="InMAGE:2769566"
/clone="InMAGE:2769566"
/clone="inMage:2769566"
/clone="organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plassmid DNA from the normalized library NoT_CGAP_Kid3 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.

Fatima Bonaldo.

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                                                                                                                                                                        tactttotggacotocacaactggaaaaatacotogaagcaatoaaaatatttotggto 519
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                                                                                                                                             90
                                                                                        Gaps
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                                                         Length 404;
                                                                                      Indels
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                                                      Query Match
13.7%; Score 404; DB 88;
Best Local Similarity 100.0%; Pred. No. 2e-202;
Matches 404; Conservative 0; Mismatches 0;
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107 c
 96
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AM304130 404 bp mRNA EST 18-JAN-2000 xs13e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2769536 3'similar to SW:XK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION: ;, mRNA sequence.

X304130 X304130 SFINITION

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ORIGIN
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BE747163
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
1 (bases 1 to 474)
1 (bases 1 to 474)
1 (bases 1, Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Y., Washu-Marck EST Project 1997,
Unpublished (1997)
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0
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to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8
INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 465.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 474;
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                        'clone_lib="Soares ovary tumor NbHOT"
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100.0%; Pred. No. 2.3e-201;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:724519"
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120 c 129 g
                                                                                                                  IN ZE37G04.S1 SOARES OVARY to IMAGE:724519 3' Similar to KD PROTEIN IN SIS2-MTD1 IN AA291670
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                                                                                                                                                                                                AA291670.1 GI:1939648
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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hes 402; Conservative
                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                     PEFERENCE
AUTHORS
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JOURNAL
JOMMENT
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                                                                                              SESULT 2.
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/tissue_type="adenocarcinoma cell line"
/lab_host="DHIOB (phage=resistant)
/nab_host="DHIOB (phage=resistant)
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
FCORI; CDNA made by oligo-dr priming. Directionally
cloned into EccNIXAOI sites using the following 5'
adaptor: GGCACGAG(G): Size=reslected >5000p for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tels: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DFP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM524 row: 1 column: 14
High quality sequence stop: 781.
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                                                                                                                 catattoctgacaogaatgcactggtctaatgttgggggcttaagttggaatgattcttac
                                                                                                                                                                                                                                                                                                                                                                                         193 CATATICCIGACACGAAIGCACIGGICIAAIGIIGGGGGCIIAAGIGGAAIGAITCIIAC
                                                                                                                                                                                                                                                                                                                                                                ccactctgccccagaatacgaggatgaaaccatgacagtttaccagatccccatacacag
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 992)
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Pred. No. 2.8e-200;
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/organism="Homo sapiens"
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/clone="IMAGE:3838237"
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99.7%; Pred
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Query Match
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Bukaryota: Metazoa; Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 574)
1 (bases 1 to 574)
1 (harba:/www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM52 row: n column: 14
                                                                                                     1551
                                                                                                                                                                                                                                                                                                                                                                                                                  BE250309 574 bp mRNA EST 13-JUL-2000 600943455F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:2960077 5'
                                                                                                                                                                    gcctcctcaagtaccagctccaggaggaggagtggcagagggatgccattattactt 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 TTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTC 149
                                                           270 GCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACTT
                                              gcagccacaagattcaaacccagctcaacctcatccacccggacatcttccccctgctca
1672 ctgtgtttgtgtcccacctgcacgcagatcac 1703
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Location/Qualifiers
1. 574
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ Clone="Image:2960077"
/ Clone="Image:2960077"
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Email: Robert_Strausberg@nih.gov
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BE250309.1 GI:9120418
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 431)
Adams, M.D.; Kerlavage, A.R.; Fleischmann, R.D.; Fuldner, R.A.; Bult
S. Adams, M.D.; Kerlavage, A.R.; Fleischmann, R.D.; Fuldner, R.A.; Bult
O.; Sutton, G.; Blake, J.A.; Brandon, R.C.; Man-Wai, C.; Clayton, R.A.;
Cline, T.R.; Cotton, M.D.; Earle-Hughes, J.; Fine, L.D.; Fitzgerald
J.M.; Fitzhugh, W.M.; Fritchman, J.L.; Geoghagen, N.S.; Glodek, A.;
Glehm, C.L.; Hanna, M.C.; Hedblom, E.; Hinkle, P.S.; Tr.; Kelley, J.M.;
Kelley, J.C.; Liu, L.I.; Marmaros, S.M.; Merrick, J.M.; Pelligrino, S.M.;
Moreno-Palanques, R.F.; McDonald, L.A.; Nguyen, D.T.; Pelligrino, S.M.;
Phillips, C.A.; Ryder, S.E.; Scott, J.L.; Saudek, D.M.; Shirley, R.;
Small, K.V.; Spriggs, T.A.; Utterback, T.R.; Weidman, J.F.; Li, Y.;
/tissue_type="rhabdomyosarcoma"
//ab_host="DH108 (phage-resistant)"
//note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; CoNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500pp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

18 c 167 g 119 t 6 others
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5' end, mRNA sequence.
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Pred. No. 8.2e-192;
0; Mismatches 1;
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EST181085 Jurkat T-cells V Homo sapiens
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99.8%;
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Matches 434; Conservative
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AUTHORS
TITLE
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Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dünke, D., Ferrie, F., Ferrie, A., Fischer, C., Hastlings, G.M., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon,
Venter, J.C.

Venter, J.C.

Initial assessment of human gene diversity and expression patterns
Dased upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 431;
                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
Fax: 3018699423
Email: arkerlavetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%; Score 380; DB 5; I 99.8%; Pred. No. 1.1e-189; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="ATCC (inhost):156306"
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/clone_lib="Jurkat T-cells V"
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                                                                                                                                                                                         Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                          Contact: Kerlavage, AR
                                                                                                                                                            Other_ESTs: THC175624
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/tissue_type="adenocarcinoma cell line"
/lissue_type="adenocarcinoma cell line"
/lab_host="npil0B (phage-resistant)"
/note="organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
25 a 263 c 281 g 179 t l others
                                                                                                                                                                                                                                                  Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenth.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM524 row: g column: 18
High quality sequence stop: 668.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BE744197 949 bp mRNA EST 15-SEP-2000
601577168F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838121 5'
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Pred. No. 5.7e-186;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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99.78;
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Matches 613; Conservative
                                                                mRNA sequence.
BE744197
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/lab_host="bH10B (phage_resistant)"
/note="Organ: utefus; Vector: pCMV-SPORT6; Site_1: Not1;
/note_"Organ: unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "

Average insert size 2.1 kb. "

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                                    BE883616 370 bp mRNA EST 27-SEP-2000
601508091F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909527 5/
mRNA sequence.
                                                                                                            cacccagcacttggtcctgaatgagaactgtgcctcagttcacaaccttcgcagccacaa 1201
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CDMA Library Preparation: Life Technologies, Inc.
CDMA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM710 row: f column: 24
High quality sequence stop: 370.
Location/Qualifiers
                                                                       299 CACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 370) MIH MGC http://www.ncbi.nlm.nih.gov/MGC/. NIH MGC http://www.ncbi.nlm.nih.gov/MGC/. National Institutes of Health, Mammalian Gene Collection (MGC)
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100.0%; Pred. No. 2.1e-184;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/clone_lib="NIH_MGC_71"
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Best Local Similarity 100.
Matches 370; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 745)
NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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2092 ccctcctgatacatgaagccaccctggaagatggtttggaagaggaagcagtggaaaaga 2151
                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                           181 IGCIGAACCACTICAGCCAGCGCTAIGCCAAGGICCCCCTCTTCAGCCCCCAACTICAGCG
                                                                                                                                                                                                                                                                                        2272 agaaagtgggagttgcctttgaccacatgaaggtctgctttggagactttccaacaatgc
                                                                                               2152 cacacagcacaacgtcccaagccatcagcgtggggatgcggatgaacgcggagttcatta
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/clone_11b="NIH_MGC_21"
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Location/Qualifiers
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Best Local Similarity
Matches 352; Conserv
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R., Williamson,A., Wohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashUrwerck Est Project
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Insert Size: 2215
High quality sequence stops: 331 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2215 Std Error: 0.00
                                                             1917
                                                                                                                                                                                                                                                                                                                                 1977
                                                                                                                               1738 aacgcgccttggcatctttgggaaagccgcttcaccctttgctggtggttgccccaaac 1797
                                                                                                                                                                                                agctcaaagcctggctccagcagtaccacaaccagtgccaggaggtcctgcaccacatca 1857
                                                                                                                                                                                                                                                                                                                                                                                               223
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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   Length 745;
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/db_xref="taxon:9606"
/clone="IMAGE:166063"
/clone_lib="Soares adult brain N2D4HB55y"
                                Indels
Query Match 12.4%; Score 368; DB 137; Best Local Similarity 100.0%; Pred. No. 2.5e-183; Matches 368; Conservative 0; Mismatches 0;
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High quality sequence stop: 331.
Location/Qualifiers
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Fax: 314 286 1810
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R87541
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28h1 Human retina cDNA randomly primed sublibrary Homo sapiens CDNA
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ORGANISM.-Homo sapiens
ORGANISM.-Homo sapiens
Contact: Chordata: Craniata: Vertebrata: Euteleostomi;
EPERENCE (Mammalla: Eutherla: Primates: Catarrhini; Hominidae; Homo.

EFERENCE (Macke, J., Smallwood, P. and Nathans, J.

TILLE Adult Human Retina CDNA
JOURNAL Unpublished (1996)
OMMENT Contact: Dr. Jeremy Nathans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 gtactcctccagatcctggtgctgcttttgtggtggtagaatgtccagatgaaagcttca 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ITCACAACCTICGCAGCCACAAGATICAAACCCAGCTCAACCTCATCCACCGGACATCT
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100.0%; Pred. No. 7.3e-175;
ive 0; Mismatches 0;
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W27286
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AA811170 396 bp mRNA EST 19-FEB-1998 ob42c03.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1334020 3',
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pGWV-SPORT6; Site_1: NotI:
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATC/DoTD/DTP
CDNA Library Preparation: LM.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM799 row: 1 column: 09
High quality sequence stop: 662.
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100.0%; Pred. No. 3.4e-172;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                 1. .790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:3920792"
/clone_lib="NIH_MGC_72"
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//dev_stage="adult"
//dev
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                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases-1 to 790)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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601435738F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920792
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   Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRimers
FORWARD: CTTTGGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAAGATT.
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                                                      David Allman,
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Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                 Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/Dbry/image/fimage.html
Insert Length: 885 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 377.
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Aorganism="Homo sapiens"
(db.xref="taxon:9606"
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/clone="lib="NGI_GGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.6%; Score 343; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 4.2e-170;
Matches 343; Conservative 0; Mismatches 0;
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
TTE1: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Kilmier, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washirotry Contact: Wilson RK.
Washirotron University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1870
Fax: 3
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AA634909 446 bp mRNA ab27h02.rl Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:842067 5' similar to SW:YK59_YEAST P36159 HYPOTHETICAL KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~ 2244 gtccccctcttcagccccaacttcagcgagaaagtgggagtt 2285
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/organism="Homo sapiens"
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BE795434.1 GI:10216632
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BE795434
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TITLE
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COMMENT
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Hillier, D., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., Walte, Y., Walte, T., Waterston, R. and Wilson, R., Theising, B., Unpublished (1997)
                                         AA679618 452 bp mRNA EST 02-DEC-1997 372612.81 Gesler Wilns tumor Homo sapiens DNA clone IMAGE:1128502 3' similar to SN:YK59 YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MIDI INTERGENIC REGION.; mRNA sequence.
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 frwd. ET from Amersham.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1128502"
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/lab_host="DH108"
                                                                                                                                  AA679618
AA679618.1 GI:2660140
                                                                                                                                                                                                                              Homo sapiens
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/lob_lost="DHIOB (phage-resistant)"
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM807 row: f column: 23
High quality sequence stop: 389.
Location/Qualifiers
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BE795434 698 bp mRNA EST 20-SEP-2000 601592991F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3946774 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                              ccactctgccccagaatacgaggatgaaaccatgacagttta 592
                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/note="Organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oilgo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected 550bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis Rit
(Stratagene) and Superscript II RT (Life Technologies)."
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Contact: Robert Strausberg, Ph.D.

Tel: (201) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 672.
345 AAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGTATGGAGCTGTGCCGAGGCTT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccgagacttaac
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                                                                    gggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccg
                                                                                                        285 GGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCTGGCACAGCCG
                                                                                                                                                                                                          225 CGGCCAGGAGGCTGCCACACGGAAGCAGATGAACTAATTTCATTTCAAGGCAGTT
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Pred. No. 2.6e-165;
0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:3835658"
/clone=lib="NIH_MGC_9"
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KEYWORDS
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/clone_lib="NH_MGC_38"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="and08 (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
/notion: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
/notion: pT73-Pac; Site_1: NotI; Si
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 345)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                          teaccetttgetggtggttgccccaaccagetcaaagectggetccagcagtaccacaa 1828
                                                                                                                                                                                                                                                                                                                                                                               ccagtgccaggaggtcctgcaccacatcagtatgattcctgccaaatgccttcaggaagg 1888
                                                                                                     gggcttgccaagtatcttgctgcagagagagacgccttggcatctttgggaaagccgct 1768
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CCAGTGCCAGGAGGTCCTGCACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGG
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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larity 100.0%; Pred. No. 1.9e-167;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/db_xref="taxon:9606"
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Gaps

Length 677; Indels

Best Local Similarity 99.8 Matches 454; Conservative

aagagcacggtcccccaggaggcagctcaggataggtggtagtaggagctgtgccgaggctt 2678

Local

Matches

2619

7

SASE COUNT

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/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 416)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
NIH-AGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theoryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM85 row: f column: 12
High quality sequence stop: 416.
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2217 aaccacttcagccagcgctatgccaaggtcccctcttcagccccaacttcagcgagaaa
                                                                                                                                                                                                                                                ctgatacatgaagccaccctggaagatggtttggaagaggaagcagtggaaaagacacac
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                                                            tattccggggacaccatgccctgcgaggctctggtccggatggggaaagatgccacctc
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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BE298273
BE298273.1 GI:9182013
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AUTHORS
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1 (Dases 1 to 940)

1 (Dases 1 to 940)

2 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

3 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

3 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

7 Tel: (301) 496-1550

5 Email: Robert_Strausbergenih.gov

7 Tissue Procurement: DCTD/Drp

6 CDNA Library Preparation: Ling Hong/Rubin Laboratory

7 CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LINL)

7 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: image.linl.gov

8 Plate: LLCM754 row: d column: 11

8 High quality sequence stop: 631.

8 Location/Qualifiers
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Pred. No. 3.3e-163;
0; Mismatches 1;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%;
99.7%;
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Best Local Similarity 99.7'
Matches 380; Conservative
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BE743831
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np66h03.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131317 3' similar to SW:XK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MT1 INTERGENIC REGION, ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGCGCACCTTTCCTCTAATCCAGCAA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2790 aaggcagtttttaaagaagtcttggaaacagacggcgcacctttcctctaatccagcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2670 ccgaggcttgggctcccacataagcactagtctatagatgcctcttaggactggtgcctg
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/clone="IMAGE:2467800"
/clone=lib="NCI_GAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2910 agacttaacgaaaatagtatttcagctgcaataaagattgagtttgcaa 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AGACTIAACGAAAATAGTATITICAGCTGCAATAAAGATIGAGTITGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 325; DB 27;
Pred. No. 1.5e-160;
0; Mismatches 4;
   www-bio.llnl.gov/bbrp/image/image.l
Insert Length: 1291 Std Error: 0
Seq primer: -400P from Gibco
High quality sequence stop: 467.
                                                                                                            /organism="Homo sapiens"
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al Similarity 99.2%;
525; Conservative
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/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="bH10B (phage-resistant)"
/note="Organ: overry; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
50 a 242 c 281 g 167 t
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DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.-G.B. Consortium/LLNL at:
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wp7e01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467800 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 511)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI/ONINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI/ONINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Oxidanal Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAP) Tumor Gen Index
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                     Ouery Match 11.1%; Score 329; DB 135; Best Local Similarity 100.0%; Pred. No. 1.2e-162; Matches 329; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mŘNA sequence.
A1937465
A1937465.1 GI:5676335
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Email: Robert_Straus
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nes 323; Conserv
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KEYWORDS
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                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/Amage/Image.html
Insert Length: 1436 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 383.
Location/Qualifiers
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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ilarity 100.0%; Pred. No. 1.7e-159;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone='IMAGE:1131317"
/clone_lib="NCI_CGAP_B12"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .397
/organism-"Homo sapiens"
/db_xref-"taxon:9606"
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100 c 111 g
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   GI:255532
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Unpublished (1997)
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                                                        Homo sapiens
   AA632118.1
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R55841 23-MAY-1995
yg860d1.r1 Soares infant brain INIB Homo saptiens cDNA clone
IMAGE:40931 5' similar to SP:XK52_XEAST P36159 HYPOTHETICAL 96.8 KD
PROTEIN IN SIS2-MTD1 INTERGENIC ; , mRNA sequence.
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1 (base; 1 to 482)
11 (base; 1 to 482)
12 (lark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T. Williamson, A., Wohldman, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 1777
High quality sequence stops: 387 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1777 Std Error: 0.00
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23-MAY-1995
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:413472"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%; Score 323; DB 144;
ilarity 100.0%; Pred. No. 1.7e-159;
Conservative 0; Mismatches 0;
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Location/Qualifiers
                                                                                                                                R55841.1 GI:825947
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Wilson RK
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/tissue_type="Choriocarcinoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: placenta; vector: poTB7; Site_1: XhoI;
/note="Organ: placenta; vector: poTB7; Site_1: XhoI;
Site_2: EcoR1; DDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following s' adaptor: GGCACGAG(G)...Size-selected >500bp
for average insert size 1:8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 206 c 203 g 157 t lothers
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Location/Qualifiers
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                                                                                                                                                                                                                                                                      366 AAGAGCTGTGTACTCCTCCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATG 307
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleoston

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

MIL-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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601677393F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3959926 {
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TWAGE:395925"
/clone_lib="NIH_MGC_21"
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Email: Robert_Strausberg@nih.gov
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TITLE
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COMMENT
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[lab_host="Dutlos"

[lab_host="Dutlos"

[lab_host="Dutlos"

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[lab_host="Organ: mixed (see below); Vector: pT7T3D-Pac

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(Dases 1 to 366)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Leh,M., Lennon,G., Marra,M., Parsons,J., Rikth,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Wailliamson,A., Wohldmann,P. and Wilson,R.

The WashU-warck Est Project
Contact: Wilson RK
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/clone="IMAGE:6606"
/clone_lib="Soares_NhHMPu_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA233087 366 bp mRNA EST 28-FEB-1997
zr68908.rl Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:668606
5′ mRNA sequence.
AA233087
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
                                                                                                                                                                                                         1670 tgctgtgtttgtgtcccacctgcacgcagatcaccacacgggcttgccaagtatcttgct 1729
                                                                                                                                                                                                                                          163 TGCCACACTTGTCAACATAAGCCCCGACACGTCTGCTACTGGACTGTGGTGAGGGCAC 222
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity 99.7
Matches 365; Conservative
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FOURCE

TEFERENCE AUTHORS

TITLE JOURNAL JAMENT

RESULT 44 RA233087/c

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ACCESSION EYWORDS source

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AUTHORS
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. Ist strand cDNA was primed
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 491)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
MashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zj67h01.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA AA676661
                                                                                                                                                          ccacacttgtcaacataagccccgacacgtctctgctactggactgtggtgagggcacat 1611
                                                                                                  1372 gcaatcctgaggaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtgc 1431
                                                                                                                 314 CCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGGGGCACAT
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/db_xref="taxon:9606"
/db_armelib="IMAGE:459985"
/clone=lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contract: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1800
                                        Length 735;
                                                                      Indels
                                         Score 307; DB 137;
Pred. No. 5.2e-151;
                                                                      ö
                              10.4%; bred. No. ...
100.0%; Pred. No. ...
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                                                                      Matches 307; Conservative
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DA576661/c
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JOURNAL
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases I to 480)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldman,P. and Wilson,R.
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R90875 480 bp mRNA EST 25-AUG-1995 yn01d02.rl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167139 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 AGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCGAGGTTGGG
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                                                                                                                                                                                                           Length 491;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                         Score 302; DB 10;
Pred. No. 2.3e-148;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I 1 121 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2922 aatagtatttcagctgcaataaagattgagtttgc 2956
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Conservative 0;
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Contact: Wilson RK
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;, mRNA sequence.

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SIS2-MTD1 INTERGENIC REGION.
                                         human
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ORIGIN
                                                 ORGANISM
        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                       AUTHORS
TITLE
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        High quality sequence stops: 263 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 4441 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1180 ttcacaaccttcgcagccacaagattcaaacccagctcaacctcatccacccggacatct 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1060 tggccttggtggttcacatggccccagcatctgtgcttgtggacagcaggtaccagcagt 1119
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                                                                                                                                                                                                                                                                                                                                                                                              Length 480;
                                                                                                                                                                                                                                                                                                                                                      8 others
                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:167139"
/clone_lib="Soares adult brain N2b4HB55y"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                            tch 10.2%; Score 301; DB 144; al Similarity 100.0%; Pred. No. 7.7e-148; 301; Conservative 0; Mismatches 0;
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                                                                             1. .480
/organism="Homo sapiens"
/db_xref="GDB:587834"
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Best Local Similarity
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National Cancer institute, Cancer Genome Anatomy Figger (Conf.), and the Confact. Robert Strausberg, Ph.D.
Contact: Robert Strausbergenih.gov
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NGI-GEP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
Info@thmage.llni.gov
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Possible reversed clone: spolyT not found
Seq primer: -400P from Gibco
High quality sequence stop: 494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="TwAGE:303219"
/clone_lib="mor_CGAP_Kid11"
/lab_host="DH10B"
/clone_lib="mor_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 agagaagggggacgtcggggtgctccggcggccaaacaccgtgtacctgcaggtggt 238
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Best Local Similarity 99.6%; Pred. No. 7.7e-148;
Matches 471; Conservative 0; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 AGAGAAGCGCGGACCGTCGGGGGTGCTCCGGCGCCCCAAACACCGTGTACCTGCAGGTGGT
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AW771657.1 GI:7703715
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AW771657 511 bp mRNA EST 04-MAY-2000 hn59h06.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032219 similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN

SFINITION

48

RESULT 4
AW771657
LOCUS

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human.
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DEFINITION
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AI174501
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=tt2=RC3-BN0036-260
400-015-e066t3=2000-04-26£t4=1)
Seq primer: puc. 18 forward
High quality sequence start: 9
High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: breast_normal; vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 297)
1 bolas Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                              AW994476 297 bp mRNA EST 05-JUN-2000
S23-BN00386-260400-015-e06 BN0036 Homo sapiens cDNA, mRNA sequence.
AW994476 GI:8254699
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
ggctgtgcggccccactctgccccagaatacgaggatgaaaccatgacagtttaccagat 598
                                                                                                         399 GGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTTTACCAGAT
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                                                                                                                                                                    599 ccccatacacagtgaacagaggagggaaagcaccaaccatggcagagtccag 651
                                                                                                                                                                                         Proc. Natl. Jead. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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93 c 82 g 62 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0036"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
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taagececgacacgtetetgetactggactgtggtgagggcacatttgggcagetgtgec 1626

1567

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/note="Vector: pspor1; Site_1: Sal1; Site_2: Not1; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dr selection. CDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dr Not1 primer for first strand synthesis generated geggeccc(t) at the 3' end of the clones. A 5' Sall adaptor was used with sequence 5'-gtogacccagegtccg-3' Resulting cDNAs were size selected (average size 2 kb), Not1 digested, and ligated into Not1/Sall-cut pspor71. Library was constructed by Dr. Manfred Gessler."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
1 (bases 1 to 404)
1 (bases 1 to 404)
1 (bases 1, to 404)
1 (b
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A142405.51 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1701344 3' similar to SW:YK59, YEAST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-MIDI INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1806
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1701344"
/clone_lib="Gessler Wilms tumor"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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Email: jmargolin@txccc.org
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                       gaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaacata 374
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                                          Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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            Length 404;
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                        Indels
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/db_xref="taxon:9606"
/clone="Ixacon:9606"
/clone_Ixb="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH108"
          9.8%; Score 291; DB 17; 1
100.0%; Pred. No. 1.5e-142;
ive 0; Mismatches 0;
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          Query Match
Best Local Similarity 100.
Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.
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"Contact: Dr. Judith F. Margolin
Human Genome Sequencing Center at Baylor College of Medicine and
Texas Children's Cancer Center
                                                                                                                                                                                                                                                                                                                                                                                                                                   cgcaccogtatctgccctccttgctggtagaagctgaagagcacggtcccccaggaggca 2642
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 414)
• Wel,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
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normalized, and was constructed
M.Fatima Bonaldo."
124 g 135 t
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                                                                                                                                          Score 290; DB 136;
Pred. No. 5.2e-142;
0; Mismatches 4;
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Tel: 713 770 4536
Fax: 713 770 4038
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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednaritk,D.T., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Runsch,C., Hungjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,W.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
                                                                                                                                                                                                Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Mature 377 (6547 Suppl), 3-174 (1995) 96056280
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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Pred. No. 6.7e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="ATCC (inhost):153799"
/db_xref="taxon:9606"
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Similarity 100.0%; Pred. No. 6.7.
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blarke, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Ciline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Handa, M.C., Heddlom, E.L., Hinkle, P.S.JT., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
                                                                                                                                                                                                                                                                  /note—Vector: lambda pSB; Site_1: BamHI; Site_2: ECORI; First strand cDNA was primed with an anchored Xhor1-Oligo(dT) primer [5'6GAGGATCGAGCGGCGCGCAGGAGGAG(T)VN 3'; V-A.C.G.; N-A.C.G.T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGACTCGGATCGGGCCGCAATAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and Xhor and directional olicod into the BamH1 and sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 agggacgcaccatatcgcaggcacccgccgccgcgagcggccgcgcaaggacccgctgc 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 ggcacctgcgcacgcgagagagcgcggaccgtcggggtgctccggcggcccaaacaccg 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 GGCACCTGCGCACGCGAGAGAGCGCGGGACCGTCGGGGTGCTCCGGCGGCGCCCAAACACCC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 TGTACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGCTCTACGTCTTCT 307
                                                                                                                    acute lymphoblastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1997
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EST61719 Activated T-cells XX Homo sapiens CDNA 5' end, mRNA
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukemia Baylor-HGSC project-TCBA"
                                                                                                                    cell
                                                                                                                                                                                  /tissue_type="leukopheresis"
/cell_type="pere B cell"
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                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="Pediatric pre-B
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         Location/Qualifiers
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AA353573.1 GI:2005893
EST.
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-2353573
-25US
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National institutes of nearin, manumatian dens contection (Mac.) other_ESTs: 2820640.5prime
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (Linu) DNA Sequencing by: Berkeley MGC Sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/Lila at:
www-bio.linl.gov/bbrp/image/timage.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Rashingtion Genome Center.
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
ptrp://www.genome.washington.edu Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
polyadenylated.
                                                                                                                                AW248468 394 bp mRNA EST 07-JAN-2000
2820640.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 3',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lung; Vector: POTBT; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 394)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2693 gcactagtctatagatgcctcttaggactggtgcctggcacagccgcggggccaggaggct 2752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 CCAGGAGGCAGCTCAGGATAGGTGCTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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  352 CICGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
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Pred. No. 7.7e-139;
0; Mismatches 2;

    .394
    /organism="Homo sapiens"

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High quality sequence stop: 213.
Location/Qualifiers
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/clone="IMAGE:2820640"
                                                                                                                                                                                                                                               AW248468.1 GI:6591461
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                                                                               RESULT 55
AW248468/c
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COMMENT
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:321917"
/clone="IMAGE:321917"
/tissue_type="parathyroid_tumor_"NbHPA"
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="parathyroid gland; Vector: pr773D (Pharmacia with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; ist strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTT-3], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                   Homo saplens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

(Dases 1 to 397)

Hillieri... Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Leh,M., Lennon,G., Marra,M., Parsons,J.,

Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston

The WashU-marck EST Project

Unpublished (1995)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: similarity on wrong strand Insert Length: 678 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 cgggactcgggcgcgcgctctacgtcttctccgagttcaaccggtatcttctaactgt 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 ggagaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaac 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 CGGGACTCGGGCGCGCGCTCTACGTCTTCTCCCGAGTTCAACCGGTATCTTCTAACTGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGCTCGCCTGGACAAC 231
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                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 285; DB 146; Length 397;
llarity 100.0%; Pred. No. 2.3e-139;
Conservative 0; Mismatches 0; Indels 0
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'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:1259575"
/db_xref="taxon:9606"
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Best Local Si
Matches 285;
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                               AI803400 489 bp mRNA EST 13-DEC-1999
tc42f03.x1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:2067293 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@iih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1275 Std Brror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 446.
Location/Qualifiers
                                  2872
                                                                                                                           2873 caagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtatttc 2932
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                                                                                                                                                94 CAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTC 35
                                                                              2813 ggaaacagacggcacctttcctctaatccagcaaagtgattccctgcacaccagaga
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
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Pred. No. 2.6e-138;
0; Mismatches 4;
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/db_xref="taxon:9606"
/clone="IMAGE:2067293"
                                                                                                                                                                       AI803400.1 GI:5368962
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Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bass 1 to 307)

Sadams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.W., Glayton,R.A.,

Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald

J.L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr.P.S., Kelley,J.M.,

Klimek,K.M., Kelley,J.C., Liu,L.I., Maymen,D.T., Pellegrino,S.M.,

Moreno-Palanques,R.F., McDonald,L.A., Nquyen,D.T., Pellegrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weilman,J.F., Li,Y.,

Bednarik,D.P., Cao, U., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,

Kunsch,C., Ji,H., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Weil, Y.-F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon

W.R.F., Wang,J.T., Wang,L., Rosen,C.M., and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T34216 307 bp mRNA EST 06-SEP-1995
EST64346 Human White blood cells Homo sapiens cDNA 5' end similar
to None, mRNA sequence.
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Contact: Venter, JC
The Institute for Genomic Research
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/note="Vector: pr7r3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7r3 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2834 teetetaateeageaaagtgatteeetgeacaeeagagaeaageagagtaaeaggateag 2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW806551 278 bp mRNA EST 17-MAY-2000 ILO-ST0002-160599-003 ST0002 Homo sapiens CDNA, mRNA sequence AW806551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgccctccttgctggtagaagctgaagagcacggtccccaggaggcagctcaggatag
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 336.
Location/Qualifiers
                                                                                                               /clone="IMAGE:925867"
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                                                                                                                                                                                                                                                                                                                                            /sex="pooled"
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information can be
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
                                                        For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammallai Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1855 tcagtatgattcctgccaaatgccttcaggaaggggctgagatctccagtcctgcagtgg 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                      1735 gagaaacgcgccttggcatctttgggaaagccgcttcaccctttgctggtggttgcccca 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1795 accageteaaageetggeteeageagtaceacaaecagtgeeaggaggteetgeaceaca 1854
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nf76f10.sl NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:925867
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Insert Length: 680 Std Error: 0.00
                                                                                                                                        l. 307
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/db_xref="taxon:9606"
/clone_lib="Human White blood cells"
/tissue_type="white blood cells"
/note="Grgan: blood"
86 g 75 t
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100.0%; Pred. No. 8.7e-138;
tive 0; Mismatches 0;
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 Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
                                                                                                               primer: M13 Reverse
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Matches 282; Conservative
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MAGE:844019 5', mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This ender on be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=LLO-ST0002-160
599-003&t2=1999-05-16&t4=1)
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2 dorcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvablo, A.F., Matsukuma, A., Balia, G.S., Simpson, D.H.,
Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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ab48b06.rl Stratagene lung carcinoma 937218 Homo sapiens CDNA clone
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                  Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
INAGE Length: 694 Std Error: 0.00
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 453.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BT0041-030999-013-e09&t3=1999-09-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 75
High quality sequence start: 75
Location/Qualifiers
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                                               AW175581 364 bp mRNA EST 16-NOV-1999
QVO-BT0041-030999-013-e09 BT0041 Homo sapiens cDNA, mRNA sequence.
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I (bases I to 364)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                               AW175581.1 GI:6441618
                                                                                                                                                                                                                                                                                                                                           rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
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a modified polylibrar; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH13W, testis NHT, and B-cell
NCL_GAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries The pools consisted of
I.M.A.G.E. Clones 297486-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
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AA994126 457 bp mRNA EST 27-AUG-1998
23-AUG-1998
23-AUG-1998
24-AUG-1998
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royally-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1193 Std Error: 0.00
Seq primer: -40ml3 fwd. Err from Amersham
High quality sequence stop: 439.
Location/Qualiflers
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AA994126.1 GI:3180671
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DEFINITION
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//issue_type="adenocarcinoma cell line"
//ib. host="DHIOB (phage-resistant)"
//ib. host="DHIOB (phage-resistant)"
//ib. host="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG, size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Strategene) and Superscript II RT (Life Technologies)."
259 c 316 g 182 t
                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM522 row. o column: 06
High quality sequence stop: 726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 TITCAGAGGIACCAAGGAAAGGCAGAIGCCCCCGIGGCTIGGIGGTICACAIGGCCCCA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 TITGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATCTGTGAGAATGCCACC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 CAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAGATT 482
                                          BE744876 984 bp mRNA EST 15-SEP-2000 601576324F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837533 5' mRNA sequence.
                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutlaria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 984 N.M. M.M. MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.8e-129;
0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3837533"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                BE744876.1 GI:10158868
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Best Local Similarity 99.5%;
Matches 436; Conservative (
                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                 Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. , , (Dases 1 to 410)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg (Ph.D.)
Email: Robert Strausberg (Ph.D.)
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. INAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 368.
AI033108 410 bp mRNA EST 28-AUG-1998 ow98908.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:1654910 3', mRNA sequence.
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                                                                                 1326 cagetcogteccaggaggagtggcagagggatgccattattacttgcaatectgaggaa
                                                                                                                          603 CAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACTTGCAATCCTGAGGAA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1654910"
/clone=lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
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99.3%; Pred. No. 1.8e-123;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                          AI033108.1 GI:3254061
                                                                                                                                                                 1386 ttcatagttgaggcgctg 1403
                                                                                                                                                                                                          663 TICATAGTIGAGGCGCIG 680
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Matches 405; Conserve
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RESULT 65 NW592223/c EFINITION

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AUTHORS TITLE

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INEMMC:

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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA716607 479 bp mRNA EST 29-DEC-1997
2g68g07.sl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:398556 3', mRNA sequence.
                                                                                                                                 401 CTGTGTGTCTTCTGCCCCACGCACGCACCCGTATCTGCCCTTCTTGCTGGTAGAAGCTGA
                                                                                                                                                                                                                                                                             2740 gggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcagtt
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                2560 ctgtgtgtcttctgccccacgcacgcacccgtatctgccctccttgctggtagaagctga
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AA716607.1 GI:2728881
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AA716607/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 450.
                                                                                                                                                     2851 gtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccga 2910
                AWD92223 461 bp mRNA EST 22-MAR-2000 hf41a01.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934408 3', mRNA sequence.
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Pred. No. 1.8e-123;
0; Mismatches 4;
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW592223.1 GI:7279399
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Best Local Similarity 99.1%;
Matches 455; Conservative
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Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 501)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,C.J., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
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                                                                                                                                                                                                                                                                                   ccacaggccaagaaggtcagagcccagtgaagatctgggagaccctgaactcagaaggct 2561
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EST182568 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                    2622 agcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggcttggg
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Pred. No. 2.1e-122;
0; Mismatches 4; Indels
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AA311855
AA311855.1 GI:1964184
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Best Local Similarity 99.1%;
Matches 453; Conservative (
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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Fenrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Wei,Y.P., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,Raymond,L., Wei,Y.P., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                         Bioinformatics
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699428
Fax: 3018699428
Fax: 3018699428
Fax: 3018699428
Fax: 3018699428
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .501

/organism="Homo sapiens"
/db_xref="ATCC (inhost):159063"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: KhoI"
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HSDHEI030 Stratagene CDNA library Human heart,
sapiens CDNA clone HEI030, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match

8.5%; Score 250; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 8.1e-121;
Matches 250; Conservative 0; Mismatches 0;
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Z17886.1 GI:30720
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Best Local Similarity 100. Matches 247; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 299)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes, M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ws18c04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2497542 3' similar to SW:YATA_SCHPO Q10155 HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accaaccatggcagagtccagaaaggcctctcagcaggctccagtccagagcgatcttcag 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 caaagtgtgtactttctggacctccacaactggaaaaatacctcgaagcaatcaaatat 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 aggatgaaaccatgacagtttaccagatccccatacacagtgaacagaggagggaagc 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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library. Cloning vector pBluescript SK(+)"
77 c 70 g 56 t
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cat#936208"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%; Score 248; DB 147; Length 299; 99.7%; Pred. No. 9e-120;
                                                                                                                                         and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                           Contact: Genzentrum Muenchen
Laboratorium fuer molekulare Biologie
Am Klopferspitz 18a,8033 Martinsried,Germany
Email: obermaier@vms.biochem.mpg.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:DOS7384E"
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                                                                                                                                                                                                                                                                               Location/Qualifiers
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Unpublished (1997)
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                                                         AUTHORS
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 625 Std Error: 0.00
Seq primer: -40pp from Gibco
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library Nor_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purfitcation, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made 1160m the same library (clonelDs 1257096-1258631, 149064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.
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                                                                                  Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 247; DB 27; L
100.0%; Pred. No. 3.1e-119;
tive 0; Mismatches 0;
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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oe91f04.s1 NCI_CGAP_Coll Homo sapiens cDNA clone IMAGE:1419007,
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Matches 415; Conserv
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2704922
Fax: +55-11-2707001
Faxi: +55-11-2707001
Famil: asimpson@ludwig.org.bx
Finis sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-TN0060-290 800-565-B02&t3=2000-08-29&t4=1)
Seq primer: puc 18 forward
High quality sequence $top: 385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev.stage="Adult"
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//dev.stage="Corgan: testis_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
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                       Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Cooldman,G.H., Carvalho,A.F., Matsukkma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveia,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 tetteagaeteegagtegaatgaaatgageeacaetteeacatggtgttageeagaga 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 TCTTCAGACTCCGAGTCGAATGAAATGAGCCACACCTTCCACATGGTGTTAGCCAGAGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggaaacttcttggtgctcaaagcaaaggagatgggcctcccagttgggacagctgccatc 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 gaatacgaggatgaaaccatgacagtttaccagatccccatacacagtgaacagaggagg 623
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Pred. No. 1e-118;
0; Mismatches 2; Indels 0
                                                                                                                                      Sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/organism="Homo sapiens"
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    AUTHORS
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429 bp

AA838624

SSULT 71 0.838624/c

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Sequencing Center
information can be
                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2838
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                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tel: (301) 496-1550

Tel: (302) 496-1550

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NOI-CGPP clone distribution informatic found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/Dbrp/image/image/image.html
Insert Length: 1787 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham

High quality sequence stop: 375.

Location/Qualifiers
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llarity 99.5%; Pred. No. 3.6e-118;
Conservative 0; Mismatches 1;
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/db_xref="taxon:9606"
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AA838624.1 GI:2913423
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Unpublished (1997)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="NT0029"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Site_1 from ORESIES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=RC6-NT0029-240 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=RC6-NT0029-240 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=RC6-NT0029-240 Seg primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
Location/Qualifiers
                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 346)
Dias Neto.E., Garcial Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W., T. Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
                                                                                                                                                         AW889463 346 bp mRNA EST 24-MAY-2000
RC6-NT0029-240400-011-B07 NT0029 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctgagatetecagteetgeagtggaaagattgateagttegetgttgegaaeatgtga 1948
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103 c 85 g 83 t
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Fax: +55-11-2707001
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Ism numeral.

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

RS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman

R, Hillier,L., Clark,N., Dubuque,T., Elliston,K., Marra,M., Parsons,J.,

Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston

R, Walliamson,A., Wohldann,P. and Wilson,R.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1800

Exa: 314 286 1800

Exa: 314 286 1800

High quality sequence stops: 215

Source: TRAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Insert Length: 490 Std Error: 0.00

Seq primer: Mi3RPl

High quality sequence stop: 215.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        H22087 414 bp mRNA EST 06-JUL-1995 3734c04.rI Soares breast 3NbHBSt Homo saplens CDNA clone IMAGE:160134 5' similar to SP:YK59_YBAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC;; mRNA sequence.
                                                                                                                     96
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2009 ggtgcacacctctggctggaaagtggtctattccggggacaccatgcctgcgaggctct
                                                                                              Score 238; DB 141; Length 414; Pred. No. 1.8e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares breast 3NbHBst" /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GDB:578554"
/db_xref="GDB:578554"
/db_xref="taxon:9606"
/clone="IMAGE:160134"
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99.7%;
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H22087.1 GI:890782
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Best Local Similarity
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Gaps 91

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Indels

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Mismatches

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ggacccgctgcgcacctgcgcacgcgagagagcgcggaccgtcggggtgctccggcgg 211
                                                            24 TITIGGIGGAGACGGCGCATGIGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACG 83
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236;
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AUTHORS
TITLE
    Matches
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/tissue_type="choriocarcinoma"
/lab_host="MIE_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="MIE_MGC_21"
/note="Organ: placenta; vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGGG(6). Size-selected 550bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM331 row: p column: 09 High quality sequence start: 4 High quality sequence stop: 615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE409312 691 bp mRNA EST 21-JUL-2000 601300940F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635576 5'
                                                                                                                                                                                                                                    289 AACTGTGGAGAAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGCTCGCCTG 230
                                                                                                                              gacaacatattcctgacacgaatgcactggtctaatgttgggggcttaagtggaatgatt 425
                                                                                                                                                                     229 GACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGGCTTAAGTGGAATGATT 170
                                                                                                                                                                                                                                                                                              486 aaatacctcgaagcaatcaaaatatttctggtccattgaaaggaatagaactggctgtg 545
  Gaps
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                                             aactgtggagaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctg
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    Indels
    1;
    Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3635576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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TERSION
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
clicles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-98679, 1101192-1101959, and 1127928-1220515).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 119 c 109 g 118 t
AI201492 439 bp mRNA EST 30-OCT-1998 4574b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943789 3',
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 439)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:1943789"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown library type
Insert Length: 717 Std Error: (
Seq primer: -400P from Glbco
High quality sequence stop: 407.
Location/Qualiflers
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/lab_host="DH10B"
                                                                                                      AI201492.1 GI:3754098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
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                                                             mRNA sequence.
                                                                                                                                                                                      Homo sapiens
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Best Local Similarity
Matches<sup>,</sup> 435; Conserv
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8.0%; Score 236; DB 107; Length 691; 100.0%; Pred. No. 2.2e-113;

Query Match Best Local Similarity

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346 agttaaaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttg 405
H14462 394 bp mRNA EST 27-JUN-1995
yl25f04.rl Soares breast 3NbHBst Homo sapiens cDNA clone
IMAGE:159295 5', mRNA sequence.
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JOURNAL
COMMENT
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AUTHORS
                                                                                                             406
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                                                                                                                                                                                          RESULT 7.
H14462/c
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KEYWORDS
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                                                               2697
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                                                                                                                                                                                                                                                                                                                     2878 agagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtatttcagctg 2937
                                                                                                                                                                                                                                                         2818 cagacggcgcacctttcctctaatccagcaaagtgattccctgcacaccagagacaagc 2877
                                                                                                                            199 ACGGAAGCAAGCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 agttcaaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcaca 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 ACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGTCTACGTCTTCTCCG 174
                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                        Neuroscience and Anatomy
Pennsylvania State University College of Medicine
500 University Drive, Hershey, PA 17033, USA
library screened by SSH and reverse Northern blot; decreased
expression in iron loading was confirmed by Northern blot.
Location/Qualifiers
2578 acgcacgcacccgtatctgccctccttgctggtagaagctgaagagcacggtccccagg
                2638 aggcagctcaggataggtggtatggagctgtgccgaggcttgggctcccacataagcact
                                                                                                                                                                                                                                                                          319 AGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACT
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7.8e-112;
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100.0%; Pred. No. 7.8
ive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                     2938 caataaagattgagtttgc 2956
                                                                                                                                                                                                                                                                                                                                                                                                                     19 CAATAAAGATIGAGITIGC 1
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Best Local Similarity 100.
Matches 233; Conservative
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SFINITION

ACCESSION VERSION VEYWORDS

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REFERENCE AUTHORS TITLE

JOURNAL

AF188525/C

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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Asses 1 to 394)

Hillieri... Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston The Washu-Marck Est Project

Unpublished (1995)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium: (info@image.llnl.gov) for further information.
Insert Length: 509 Std Error: 0.00
Seq primer: Ml3RPI
High quality sequence stop: 268.
High quality sequence stop: 268.

Location/Qualifiers
I. #394
/ Ab_Rref="Robe:578182"
/
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/lab_host="DH10B (ampicillin resistant)"
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100.0%; Pred. No. '8.1e-112;
tive 0; Mismatches 0;
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source

FEATURES

BASE COUNT CRIGIN

226

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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                AA522537 865 bp mRNA EST 20-AUG-1997 ni38e08.sl NCI_CGAP_Lul Homo sapiens cDNA clone IMAGE:979142 3'
                                                         gattettaetttaaaggaaacegggetteeaaagtgtgtaetttetggaeeteeaeaaet 481
                                                                                                                     541
               233 CCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAAT 174
                                                                                      173 GATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACT 114
                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Bmall: Robert_Strausbergenih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                             7.8%; Score 232; DB 8; Length 865;
llarity 99.5%; Pred. No. 2.9e-111;
Conservative 0; Mismatches 1; Indels
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 436.
Location/Qualifiers
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235 c 227 g 218 t
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/db_xref="taxon:9606"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                 mRNA sequence.
AA522537
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Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tabal: Robert Strausberg@hih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbry/image/image.html

Insert Length: 846 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 255.

High quality sequence stop: 255.

Irce

1. 282
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8 6 8 6 9 84 t lothers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 282)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                       2719
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                                                                                                                                                                                                                                                                                                                                                                         AA928608 282 bp mRNA EST 07-JUL-1998
om75b03.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552973
mRNA sequence.
AA928608
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                                                                                                                                                                                                                                              2600 teettgetggtagaagetgaagageacggteeeceaggaggeageteaggataggtggta
                                                                                                                          tggagctgtgccgaggcttgggctcccacataagcactagtctatagatgcctcttagga
                                                                                                                                                                                 283 recadentereceasecriseserrecearanasecriatrasargarecerrangea
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/db_xref="taxon:9606"
/clone="INAGE:552973"
/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA928608.1. GI:3076899
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Unpublished (1997)
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63 a

BASE COUNT

403 GAGACCCIGAACTCAGAAGGCIGTGTGTCTTCTGCCCCACGCACGCACCCGTATCTGCCC 344

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BASE COUNT
ORIGIN
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AI357786/C
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TITLE
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I (Dassa 1 to 282)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Kilmek, K.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weider, D.P., Lischer, C., Hastings, G.A., He, W.-W., Huj, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weiter, T., Rosen, C.M., and
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Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tabinfoetdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 bp mRNA EST 06-SEP-1995
Human White blood cells Homo sapiens CDNA 5' end similar
                                                                                                                                                                                                 228 GCACAGCCGCGGCCCAGGAGCTGCCACACGAAGCAAGCAGAATGAACTATCATTTC 169
                                                                                                                                                                                                                                                                      Length 282;
                                                                                                                                                                                                                                                                                                                                                 2910 agacttaacgaaaatagtatttcagctgcaataaagattgagtttgca 2957
                                                                                                                                                                                                                                                                                                                                                                  Score 228; DB 13; I
Pred. No. 3.5e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .282
/organism="Homo sapiens"
/db_xref="ATCC (inhost):104694"
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                                            7.7%; Scor.
100.0%; Pred. No. 3...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20
Trel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (tdbinfo@tdb.tigr.org)
Seg primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 377, 3-174 (1995)
96026280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T34024
T34024.1 GI:616122
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                      Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T34024
EST61387 B
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                                                         Query Match
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI357786 433 bp mRNA EST 15-FEB-1999 qu98d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1980109 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: Stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostom1;
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/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="Pall0B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                                                                                 1672 ctgtgtttgtgtcccacctgcacgcagatcaccacagggcttgccaagtatcttgctgc 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1732 agagagaacgcgccttggcatctttgggaaagccgcttcaccctttgctggtggttgccc 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AGAGAAGGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CTGTGTTTGTGTCCCCCCCCCGCAGGCAGACACCACACAGGCTTGCCAAGTATCTTGCTGC 85
                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                               Length 282;
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/db_xref="taxon:9606"
/clone_lib="Human White blood cells"
/tissue_type="white blood cells"
/note="Corgan: blood" 62 t 2 of
                                                                                                                                                                                                                               7.7%; Score 228; DB 145;
100.0%; Pred. No. 3.5e-109;
iive 0; Mismatches 0;
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Insert Length: 2467 Std Error: 0.00
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/db_xref="taxon:9606"
/clone="IMAGE:1980109"
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High quality sequence stop: 397.
Location/Qualifiers
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Unpublished (1997)
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AI357786
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Best Local Simi
Matches 228;
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97044478
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ORIGIN
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COMMENT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gatcagtgggtctaagtgtccgagacttaacgaaaatagtatttcagctgcaataaagat 2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE615669 872 bp mRNA EST 24-AUG-2000 601279347F1 NIH_MGC_39 Homo sapiens cDNA cione IMAGE:3611338 5'
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                                                                                                                                                                                                                                                                                                                                              tgcctcttaggactggtgcctggcacagccgcgggccaggaggctgccacacggaagcaa 2767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)' DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                            cogtatctgccctccttgctggtagaagctgaagagcacggtccccaggaggcagctca
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                                                                 Length 433;
                                                                                                     Indels
                                                                   Score 227; DB 19;
Pred. No. 1.2e-108;
                                                                                                     0; Mismatches
 119
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Plate: LLCM268 row: n column: 11
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/db_xref="taxon:9606"
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BE615669.1 GI:9897268
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AUTHORS
TITLE
JOURNAL
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 291)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Fucaba,T., Lacy,M., Le,M., Le,N., Mardis,E.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor NbHOT Homo sapiens cDNA clone to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8 INTERGENIC REGION: ;, mRNA sequence.
/tissue_type="adenocarcinoma"
//lab_host='DH10B (phage-resistant)"
/note="Organ: pancreas; vector: pOTB7; Site_1: XhoI;
Site_2: EccNI; cDNA made by oligo-dT priming.
Directionally cloned into EccNIXhoI sites using the following S' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found insert Length: 1829 Std Error: 0.00 Seq primer: 41ml3 fwd. ET from Amersham High quality, sequence stop: 271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 atgcaggagcacaagttaaaggttgctcgcctggacaacatattcctgacacgaatgcac
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 224; DB 110;
Pred. No. 5e-107;
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                                                                                                                                                                                                                                                                                                         257
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zt29911.s1 Soares ovary
IMAGE:723812 3' similar
KD PROTEIN IN SIS2-MTD1
                                                                                                                                                                                                                                                                          Technologies)
239 c
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224; Conservative
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polyllnker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
teaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
subtraction by Bento Soares and M. Fatima Bonaldo. "
130 c 120 g 133 t 1 others
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 228)
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98.9%; Pred. No. 6.3e-105;
tive 0; Mismatches 5;
                                                      /organism="Homo sapiens"
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High quality sequence stop: 458 Location/Qualifiers
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Matches 470; Conservative
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 876 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1804749 477 bp mRNA EST 07-MAR-2000 ML42402.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253699 3', MRNA sequence. A1804749
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 tggagaaggcgttcagaagactcatgcaggagcacaagttaaaggttgctcgcctggacaa 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ccgggactcgggcgcgctctacgtcttctccgagttcaaccggtatcttctaactg 310
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                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 221; DB 4; Length 291; 100.0%; Pred. No. 1.8e-105; Live 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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/clone=11b="Soares ovary tumor NDHOT"
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Matches 221; Conservative
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N36229 448 bp mRNA EST 16-JAN-1996 Y370cO4.s1 Soares melanocyte ZNDH HOMD sapiens CDNA Clone IMAGE:272742 3' similar to SW1559 YESS_PESST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. [1] ;, mRNA sequence.
121 GGGGCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGC 180
                                                                                     181 GTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGC 218
                                                      321 gttcagagactcatgcaggagcacaagttaaaggttgc 358
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N36229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /done="IMAGE:27305021"
/clone="IMAGE:27305021"
/clone="Image:2730-pag (Table Technologies)"
/lab.host="DH10B (Life Technologies)"
/lab.host="DH10B (Life Technologies)"
/note="Vector: pr773D-Pag (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BW, which consists of
a mixture of four normalized libraries: NCI_CGAP_Sub6
library had 7 million recombinants. A single-stranded DNA
preparation of BW was used as a tracer in a subtractive
hybridization with a driver comprising: the IMAGE pool
NCI_CGAP_Lui3 pool 1 LLAM 334-3377, 3682-3683,
3798-3803 (ImAGE ClonelDS 132376-1323911,
1456008-1456775.150552-15022855); NCI_CGAP_Kid5 pool 1
LLAM 338-3342,3722-3752, 3776-3778 (IMAGE ClonelDS
1323912-132381, 1471368-1472903, 1491104-14923255);
NCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
nCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
nCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
s1062-3608-146704-1465064-1465064-1465625, 1446964-144531
); NCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
s1062-20615); NCI_CGAP_CO10 pool 1 LLAM 2467-2459,
s1062-20615); NCI_CGAP_CO10 pool 1 LLAM 2467-2559,
s10616-2710535) and NCI_CGAP_Sub2 (IMAGE ClonelDS
s1065-2710535) and NCI_CGAP_Sub2 (IMAGE ClonelDS
s1065-2710535) and NCI_CGAP_Sub2 (IMAGE ClonelDS
s1065-2712455) (20% of the driver population).
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAGE_LIBROIL GAP-Lu13
                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
11s likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: Mi3 Forward
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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TAG_SEQ=GCCGG"
                                                Tumor Gene Index
Unpublished (1997)
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Matches 218; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

( basa 1 to 448)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldman,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
High quality sequence stops: 365
Source: IMAGE Consortium, LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: ml3 -40 forward
High quality sequence stop: 365.
Location/Qualifiers
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0
                                                                                                                                                                                                                                        Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 218; DB 142;
ilarity 100.0%; Pred. No. 7.2e-104;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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N36229.1 GI:1157371
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                                                              Homo sapiens
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145 TGGAAACAGACGGCGCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACACAGAG 86
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue: Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 239.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                      AW511765 316 bp mRNA EST 03-MAR-2000 xu76f03.xl NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807645 3',
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                   372 atattoctgacacgaatgcactggtctaatgttgggggcttaagtggaatgattcttact
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Pest Local Similarity 99.6%; Pred. No. 9.3e-102;
Matches 264; Conservative 0; Mismatches 1;
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1. 249

/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="Intaxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW247380 249 bp mRNA EST 07-JAN-2000
2820640.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 5',
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2872 acaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtattt 2931
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100.0%; Pred. No. 3.6e-100;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other ESTs: 2820640.3prime
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inih.gov
                                                                                                                                                                                            2932 cagctgcaataaagattgagtttgc 2956
                                                                                                                                                                                                                                               CAGCTGCAATAAAGATTGAGTTTGC 1
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AW247380.1 GI:6590373
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-HT0217-
201199-022-h08&t3=1999-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 74.
                                                                                                                                                                                                                                                                                                       AW378247 650 bp mRNA EST 04-FEB-2000
RC1-HT0217-201199-022-h08 HT0217 Homo sapiens CDNA, mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                              121 aggcacccgcccgccgcgagcggccgcgcaaggacccgctgcggcacctgcgcacgcgag 180
tttgctcgctgctgcggtccgcgggccggacgcaccatgtcgcagggacgcaccatatcgc 120
                                      80 TITECICGCIGCIGCGGICCGCGGCCGGACGCACCAIGICGCAGGGACGCACCAIAICGC 139
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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ilarity 100.0%; Pred. No. 4.3e-99;
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                                                                                                                                                                                                                                                                                                                                                              AW378247.1 GI:6882906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 219)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Cente information can
                                                                                                                                                                                                        AASO4146 219 bp mRNA EST 18-AUG-1997
aa59e06.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825250 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 IGCCACACGGAAGCAAGCAGATGAACTITCATITCAAGGCAGTITITAAAGAAGICI 150
459 GCGGCAGGTGCGGGCGCCCTCCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGA 400
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer. 440ml3 fwd. ET from Amersham
High quality sequence stop: 175.
Locatiod/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                           mRNA sequence.
AA504146
AA504146.1 GI:2240306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo, Ph.D
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1021 ccacctttcagaggtaccaaggaaag 1046
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R51138.1 GI:813040
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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JOURNAL
COMMENT
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VERSION
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AUTHORS
                                                                                                  901
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pr7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikih,L., Rohling,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 678 Std Error: 0.00
                                                                  2872 acaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtattt 2931
       159 TGGAAACAGACGGCGCCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACACAGAG 100
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="parathyroid tumor"
dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens'/db_xref="GDB:1259575"
                                                                                                                                                                                                        2932 cagctgcaataaagattgagtttgcaa 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone="IMAGE:321917"
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                                                                                                                                                                                                                                           Seq primer: mob.REGA+ET.
Location/Qualifiers
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Contact: Wilson RK
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KEYWORDS
SOURCE
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EATURES

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Entargota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 472)

1. (Dases 1 to 472)

2. Hilleri., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldmann,P. and Wilson,R.

7. Williamson,A., Wohldmann,P. and Wilson,R.

7. WashUngton RK

7. WashIngton University School of Medicine

7. Washington University School of Medicine

7. Tal 286 1800

7. Fax: 314 286 1800

8. Fax: 314 286 1800

9. Fax: 314 286 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                       tcactcatgaaggaagagattttggctgaagagctgtgtactcctccagatcctggtg
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100.0%; Pred. No. 8.4e-94;
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/clone_11b="Soares infant brain INIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:411293"
/db_xref="taxon:9606"
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High quality sequence stop: 327
Location/Qualifiers
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Best Local Similarity
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Bioinformatics
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MEDLINE
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AA346268
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                    AI141263 416 bp mRNA EST 05-OCT-1998
qa46h05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1689849
3', mRNA sequence.
AI141263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomn. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 416)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"

    2557 aggetgtgtgtcttctgccccacgcacgcacccgtatctgccctccttgctggtagaagc 2616

                                                                                                                                                                         1550 tgccacacttgtcaacataagccccgacacgtctctgctactggactgtggtgagggcac 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Imail: Nobert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 71 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 233.
Location/Qualifiers
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0; Indels
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Pred. No. 2.8e-93;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IXAAGE:1.68949"
/clone_11b="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches.
Mismatches
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                                                                                                                                                                                                                                              1610 atttgggcagctgtgccgt 1628
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                                                                                                                                                                                                                                                                             223 ATTIGGGCAGCTGTGCCGT 241
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.0
Matches 398; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
Matches 199;
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                                                                                                                                                                                                                                                                                                                                    ESULT 93
                                                                                                                                                                                                                                                                                                                                                                     COCUS
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dassa 1 to 394)

I (Dassa 1 to 394)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Fitchugh, W.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

J.L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Glodek, A.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Pelligrino, S.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Badnarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Hu, J.S., Greene, J.M., Gruber, C., Hastings, G.A., He, M.W.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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Initial assessment of human gene diversity and expression patterns
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9712 Medical Center Drive, Rockville, MD 20850 USA
19712 Medical Center Drive, Rockville, MD 20850 USA
19713 Medical Center Drive, Rockville, MD 20850 USA
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
email: arkerlav@tigr.org
information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                     2676
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                                                                                                         tgaagagcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggc
                                                                                                                                          2677 ttgggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagc
                                                                                                                                                                                                                                                                                296 TIGGGGTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 TGCGGGCCAGGAGGCTGCCACACGGAAGCAAGCAGGATGAACTAATTTCATTTCAAGGCAG
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EST52407 Greater omentum IV Homo sapiens cDNA 5' end, mRNA
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Nature 377 (6547 Suppl), 3-174 (1995)
96026280
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Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-23e06
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Best Local Similarity
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1 (Dases 1 to 276)

1 (Dases 1 to 276)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N.H., Kirknes; E.F., Weinstock, K.G., Gocayne, J.D., White C.J., Lee, N.H., Kirknes; E.F., Weinstock, K.G., Gocayne, J.D., White C.J., Lee, N.H., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., Glodek, A., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Ferile, A., Fischer, C., Hastings, G.A., He, W.W., Kunsch, C., Hung, J., Xu, C., Yu, G.L., Kuben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA378232 276 bp mRNA EST 21-APR-1997
EST90926 Synovial sarcoma Homo sapiens CDNA 5′ end, mRNA sequence.
AA378232
                                                                      1683 tcccacctgcacgcagatcaccacacgggcttgccaagtatcttgctgcagagagaacgc 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 TCCCACCTGCACGCAGATCACCACACGGCTTGCCAAGTATCTTGCTGCAGAGGAACGC 136
                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                   Length 394;
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                   Query Match 6.5%; Score 193; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.3e-90;
Matches 193; Conservative 0; Mismatches 0;
              Location/Qualifiers
1. 394
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: EST114300 THC175624
Seq primer: M13 Reverse.
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1 (bases 1 to 290)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html) seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="synovial membrane"
/dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2011 tgcacacctctggctggaaagtggtctattccggggacaccatgccctgcgaggctctgg 2070
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Genethon Centre de recherche sur le Genome Humain
1, rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                            1. 276
/organism="Homo sapiens"
/db_xref="ArC (inhost):182644"
/db_xref="taxon:9606"
/clone_lib="Synovial sarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 184; DB 6;
Pred. No. 7.2e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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Single read.
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          79 9
Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.2%;
Best Local Similarity 99.6%;
Matches 234; Conservative
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TITLE
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                                                                                                                                                    /tissue_twpe="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corgan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female: dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, N.N.A.S in press" 3 others
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I (bases 1 to 424)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High qality sequence stops: 315
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 TITCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGCCCCA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H03318 424 bp mRNA EST 20-JUN-1995 yj47e10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151914 3', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 182; DB 147; Length 290; 100.0%; Pred. No. 8.3e-85; tive 0; Mismatches 0; Indels 0
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/sex="Female"
                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
Seq primer: (-21)M13_universal.
Location/Qualifiers
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H03318.1 GI:866251
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Matches 182; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project; (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 749 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI033342 482 bp mRNA EST 28-AUG-1998 ox02d12.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:1655159 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2762 aagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaacaga 2821
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Best Local Similarity 100.0%; Pred. No. 8.5e-85;
Matches 182; Conservative 0; Mismatches 0;
Std Error: 0.00
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Location/Qualifiers
                                                                                                                                        /db_xref="taxon:9606"
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                                                                                                                                                                       6.1%; Score 179; DB 110;
100.0%; Pred. No. 3.4e-83;
ative 0; Mismatches 0;
                                                                                                           149 t
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High quality sequence stop: 335
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Insert Size: 954
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189 c
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bistryctus in Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k column: 08
High quality sequence stop: 577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2562 gigitoticigococacgoacgoaccogiatotgocotocitgoiggiagaagoigaag 2621
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                           /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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             /organism≂"Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:3876223"
                                            /clone="IMAGE:1655159"
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DENKATYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 376.)
Hillier; L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Wohldmann, P., Waterston, R., Wilson, R. and Maira, M.
Generation and analysis of 280,000 human expressed sequence tags
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2654 giggialgagotgigocgaggottgggotoccacalaagcactagictalagaigotic 2713
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c65b06.rl Stratagene liver (#937224) Homo sapiens CDNA clone
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                   Length 577;
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/sex="male"
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Tearch completed: February 18, 2001, 09:27:24 class: 14671 sec